

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 16:43:13 ; Search time 21 Seconds
(without alignments)
3105.612 Million cell updates/sec

Title: US-10-063-688-34

Perfect score: 3502

Sequence: 1 MRLVLTAKASVEMFLVLL.....QYVRIIIONICTFNSQPRN 678

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554	15.8	3124	2 A40020	collagen alpha 1(X
2	504.5	14.4	3137	2 A37797	collagen alpha 3(V
3	501.5	14.3	496	2 A37979	cartilage matrix p
4	490	14.0	493	2 A33809	cartilage matrix p
5	490	14.0	500	2 S66522	cartilage matrix p
6	471.5	13.5	3176	2 CGHU3A	collagen alpha 3(V
7	331	9.5	1857	2 S31212	collagen alpha 1(X
8	331	9.5	1888	2 S78476	collagen alpha 1(X
9	329.5	9.4	2944	2 A54849	collagen alpha 1(V
10	329	9.4	1747	2 A45974	collagen alpha 1(X
11	314.5	9.0	567	2 T28797	hypothetical prote
12	298	8.5	741	2 T46488	hypothetical prote
13	280.5	8.0	929	2 T51027	type XII collagen
14	279	8.0	3051	2 S42373	hypothetical prote
15	266	7.6	2813	1 VWHU	von Willebrand fac
16	262.5	7.5	843	2 A40970	undulin 1 - human
17	252.5	7.2	1019	1 A32856	collagen alpha 1(V
18	231	6.6	1153	1 RWHU1B	cell surface glyco
19	229	6.5	550	2 T23760	hypothetical prote
20	229	6.5	1153	2 S00551	leukocyte surface
21	228	6.5	1163	1 RWHU1C	cell surface glyco
22	226.5	6.5	427	2 G00039	von Willebrand fac
23	226.5	6.5	1025	2 S34839	collagen alpha 1(V
24	213.5	6.1	414	2 P50323	von Willebrand fac
25	213.5	6.1	1286	2 A88396	protein M01B10.2 [
26	210.5	6.0	2098	2 T18397	protein CTRP - mal
27	209.5	6.0	1022	2 S04111	collagen alpha 2(V
28	209	6.0	918	2 S23377	collagen alpha 2(V
29	205	5.9	1028	1 CGHU1A	collagen alpha 1(V

30	205	5.9	1029	1 S21369	collagen alpha 2(V
31	204	5.8	13055	2 T16580	hypothetical prote
32	203.5	5.8	1170	2 S03308	cell surface glyco
33	203.5	5.8	1180	2 A35854	integrin alpha-1 c
34	200	5.7	238	2 C35243	collagen alpha 2(V
35	200	5.7	917	2 S09646	collagen alpha 2(V
36	200	5.7	1018	1 CGHU2A	collagen alpha 2(V
37	195	5.6	1163	2 T56126	lymphocyte fuction
38	193	5.5	1151	2 A45226	integrin alpha-1 c
39	188.5	5.4	272	2 A55348	integrin alpha-1 c
40	187.5	5.4	1170	2 T45914	integrin alpha 2 s
41	184.5	5.3	643	2 T19549	hypothetical prote
42	182.5	5.2	1181	2 A33998	integrin alpha-2 c
43	178	5.1	763	2 T50807	complement factor
44	171	4.9	712	2 A45638	immunodominant mic
45	170.5	4.9	1178	2 S44142	VLA-2 protein homo

ALIGNMENTS

RESULT 1

A40020

collagen alpha 1(XII) chain precursor - chicken

N:Alternate names: fibrochimerin

C:Species: Gallus gallus (Chicken)

C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 15-Sep-2003

C:Accession: A40020; A34485; B3485; A28037; S23814; S22254; S28811

R:Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obar

J. Cell Biol. 115, 209-221, 1991

A:Title: The complete primary structure of type XII collagen shows a chimeric molecule w
nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.

A:Reference number: A40020; MUID:92011862; PMID:1918137

A:Accession: A40020

A:Molecule type: mRNA

A:Residues: 1-3124 <YAM>

A:Cross-references: GB:D00824; NID:G222810; PIDN:BA00701.1; PID:G222811

A:Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and,

R:Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.

J. Biol. Chem. 264, 19772-19778, 1989

A:Title: Type XII collagen. A large multidomain molecule with partial homology to type I

A:Reference number: A34485; MUID:90062079; PMID:2584192

A:Accession: A34485

A:Molecule type: mRNA

A:Residues: 2456-2758, 'A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>

A:Cross-references: EMBL:J05137; NID:G211284; PIDN:AAA48635.1; PID:G211285

A:Accession: B34485

A:Molecule type: Protein

A:Residues: 2772-2792;2846-2873 <GOR2>

R:Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.

Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987

A:Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA c

A:Reference number: A28037; MUID:87317590; PMID:3476925

A:Accession: A28037

A:Molecule type: mRNA

A:Residues: 2960-2976, 'F', 2978-3074, 'AG', <GOR3>

A:Cross-references: EMBL:M17375; NID:G211649; PIDN:AAA48718.1; PID:G211650

A:Note: this sequence has been revised in reference A34485

R:Koch, M.; Bernasconi, C.; Chiquet, M.

Eur. J. Biochem. 207, 847-856, 1992

A:Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of

A:Reference number: S23814; MUID:92362621; PMID:1323460

A:Accession: S23814

A:Molecule type: protein

A:Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517 <

R:Dublet, B.; van der Rest, M.

J. Biol. Chem. 262, 17724-17727, 1987

A:Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-

A:Reference number: S22254; MUID:88087065; PMID:3121603

A:Accession: S22254

A:Molecule type: protein

A:Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB>

R:Trueb, J.; Trueb, B.


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Db 99 KAEELQAVQRIEPLSTGTMGLAIQFAISRAFSOTEGARLSRNINKVAIVTDTGRPDQG 158
Qy 410 VEEASRLARESGINIFFI-----TIEGAARENKQYVVEPNFANK---AV 450
Db 159 VQDVASARAGAGIEFAIGVGRVDMHTLRQIASEPLDHDVYVESYVIEKLTHTKQEPAP 218
Qy 451 C-----RTNGFYSLHVOSWFLGHLTKTLQPLVKRVCDTDLRACSKTCLN 492
Db 219 CVVSDLCATGDHDCQICISTPGSYKCACKEGTFLAND-----GKTCS-----ACSGSGS 269
Qy 493 SADIGFVIDGSSSVGTGNFTVLQFVTNLTKBPEISDTRIGAVQVYTYEQRLEFGDKY 552
Db 270 ALDLVFLIDGSKSVRENFELVKKFINQIVESLEVEKQAGVGLVQYSSSVRQEPPLQGF 329
Qy 553 SSKPDILNAIKRYGYSGGTSTGAANFALEOLF---KKSHPNKRKLMILITDGRSYDDV 609
Db 330 KNKKDIKAAVKQWAYMEKGTMTGQALKYLVDSFSFANGARPGVPKVGIVFTDGRSQDYI 389
Qy 610 RIPMAAHLKGVITYAIGVAAQAQBELEVIATIPADHSPFVDFPNLHQYVPRITQNIC 669
Db 390 TDAAKGAKDLGFRMFVAGVNAVEDELREITASBPVAEHYFTADPRTISNIGKKLQMKIC 449
Qy 670 TE 671
Db 450 VE 451

RESULT 5
S66522
catilage matrix protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 28-Jul-2003
C;Accession: S66522
R;Azodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Eur. J. Biochem. 236, 970-977, 1996
A;Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein
A;Accession: S66522
A;Reference number: S66522; MUID:96270751; PMID:8665920
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-500 <AS2>
A;Cross-references: EMBL:U35035; NID:g1163178; PIDN:AAB06521.1; PID:g1163179
C;Genetics:
A;Gene: CMP
C;Superfamily: matrilin; EGF homology; von Willebrand factor type A repeat homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-500/Product: cartilage matrix protein #status predicted <MAT>
F;43-210/Domain: von Willebrand factor type A repeat homology <VWA1>
F;231-266/Domain: EGF homology <EGF>
F;277-441/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 14.0%; Score 490; DB 2; Length 500;
Best Local Similarity 28.8%; Pred. No. 4.1e-25;
Matches 130; Conservative 72; Mismatches 184; Indels 66; Gaps 8;

Qy 266 SLGLVPKKEELSTQSLPVLGDPNCKTDLSPFLIDGTSIGKRPRIOKQLLADVAAQALDI 325
Db 27 SLSLVPQQRHLCKTRPT-----DLVFWVDSRSRVPVEPKVKVFLSVIESLDV 77

Qy 326 GPAGPLMGVQYQGNPATFNKLTHTNSRDLTKTAIEKLTORGGLSNVGRASIVTNRNFFS 385
Db 78 GPNATRVGLVNYASTVKPEPFLRAHGSKASLLQAVRRIQPLSTGTGTMGLAQFAITKALS 137

Qy 386 KANGNRSGAPN---VVVMVVDGWPTDVEEASRLARESGINIFITTEGAAREN--KQYV 440
Db 138 DAEGGRARSFDISKVIVVTDGRPDQSDVRDSEERASAGIELFAIGL-GRVDRATLRQIA 196

Qy 441 VEPNFAKVCRTNGFYSLHVQSWFLGHLTKLQ-----LVKRVCDTDLRACSKTCLNS- 493
Db 197 SEQDQERVD-----YVESYNYVIEKLAKEKQFAFCVVSQDLCATGDHDCQELCVSSP 246

Qy 494 -----ADIGFVIDGSSSVGTGNFTVLQFVTNL 522
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Db 247 GSYTCACHEGFTLNSDKTCNVCRCGSGSATDLVFLIDGSKSVRPNFELVKKFINQIV 306
Qy 523 KEFEISDTRIGAVQVYTYEQRLEFGDKYKSSKPDILNAIKRVGYTSGGTSTGAANFAL 582
Db 307 DTLDVDRLAQVGLVQYSSSIRQEPFLGRFHSKKDIKARVRNMSYMEKGTMTGAALKYLI 366
Qy 583 BQLPKKS---KPNKRKLMILITDGRSYDDVRIIPAMAHLKGVITYAIGVAAQAQBELEVI 639
Db 367 DNSTVSSGARPOAQKGVIVFTDGRSQDYINDAARKAKDLGPKMFAVGVGNVVEELREI 426
Qy 640 ATPHARDHSPFVDFPNLHQYVPRITQNICTE 671
Db 427 ASEPVAHDHYFTADPRTINQIGKKLQKQICVE 458

RESULT 6
CGHJ3A
collagen alpha 3(VI) chain precursor (validated) - human
N;Contains: collagen alpha 3(VI) chain, splice form A9/N10(-)
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 12-Nov-1999 #text_change 15-Sep-2003
C;Accession: A59140; S13679; S24465; A57083; S28776; S00245; C31952; C29848; S26510; S4;
R;Chu, M.L.
submitted to GenBank, May 1998
A;Reference number: A59140
A;Accession: A59140
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-3176 <CHU>
A;Cross-references: GB:X52022; NID:g3127925; PIDN:CAA36267.1; PID:g3127926
R;Chu, M.L.; Zhang, R.-Z.; Pan, T.; Stokes, D.; Conway, D.; Kuo, H.J.; Glanville, R.; Ma;
EMBO J. 9, 305-339, 1990
A;Title: Mosaic structure of globular domains in the human type VI collagen alpha-3 chain
itors.
A;Reference number: S13679; MUID:90151612; PMID:1689238
A;Accession: S13679
A;Molecule type: mRNA
A;Residues: 1-30,237-313, 'CWV', 318-322, 'AR', 326-1815, 'PD', 1818-1819, 'ID', 1822-3176 <CHS>
A;Cross-references: EMBL:X52022; NID:g3127925
A;Accession: S24465
A;Molecule type: protein
A;Residues: 574-585;965-2018-2037;2374-2410;2445-2459;2466-2469, 'X', 2471-2474;2504-2508, 'X',
1982, 'X', 1964-1965;2018-2037;2374-2410;2445-2459;2466-2469, 'X', 2471-2474;2504-2508, 'X',
R;Zanussi, S.; Doliana, R.; Segat, D.; Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 267, 24082-24089, 1992
A;Title: The human type VI collagen gene. mRNA and protein variants of the alpha3 chain
A;Reference number: S28776; MUID:93054780; PMID:1339440
A;Accession: A57083
A;Molecule type: DNA
A;Residues: 310-328 <ZAN>
A;Accession: S28776
A;Molecule type: mRNA
A;Residues: 32-126, 'AK', 129-136, 'L', 138-236 <ZA2>
A;Cross-references: GB:S49432; NID:g260296; PIDN:AAB24261.1; PID:g260297
R;Chu, M.L.; Mann, K.; Deutzmann, R.; Pribula-Conway, D.; Hau-Chen, C.C.; Bernard, M.P.
Eur. J. Biochem. 168, 309-317, 1987
A;Title: Characterization of three constituent chains of collagen type VI by peptide se
A;Reference number: S00126; MUID:88029444; PMID:3665927
A;Accession: S00245
A;Molecule type: mRNA; protein
A;Residues: 2024-2046;2092-2156, 'R', 2203-2208, 'X', 2210-2211, 'X', 2213-2227;2228-2251;2311
A;Cross-references: GB:X06196; NID:g30055; PIDN:CA29557.1; PID:g1335034
R;Chu, M.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; Deutzmann, R.; Timpl, R.
J. Biol. Chem. 263, 18601-18606, 1988
A;Title: Amino acid sequence of the triple-helical domain of human collagen type VI.
A;Reference number: A31952; MUID:89066644; PMID:3198591
A;Accession: C31952
A;Molecule type: mRNA
A;Residues: 2038-2373 <CH4>
A;Cross-references: GB:J04211; GB:M20778
A;Note: parts of this sequence were determined by protein sequencing
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Db 713 IVGTTAIPPT-----VTTTTTATTPKPTIAVFR-----GVRNLVIDDETSS 757
Qy 228 ---LWSTATVTSQNR-----PRADPGIQDPGSAAFQKPVGVADSLGLVPKEELS 276
Db 758 LRVVWIDSHNAQQPFTVYLTAKGDRABEAIMVPGRQNTLLQP-----LLPDTYK 809
Qy 277 TQSL-----EPVSLGDPNCKIDLSPIDGSTSIGKRRFRIQKQLADVAQALDIGPAGP 330
Db 810 VTIITPIYADGEGVSAPGKTLPLS-----APNRLVSDWYNNRLRISM-APPSP 859
Qy 331 LAG--VVQYGDN---PATHFNKATHNSRDLKTAIEKIQORGLSNVGRASIVTKNFFS 385
Db 860 TMGYRIVYKSIINVPGA---LFTFVG-DINTIL-----ILNLFSGTETYSVKVPAS 906
Qy 386 KANG---NRSGAPNVVWVDGHPDTKVEASRLAR---ESGINIFITIEGAENKQY 439
Db 907 YSTGFSDALTGVAKTLYLGVNTLDTYQVRMTSLCAQMLHRHATAYRVVIESLVGKKQ- 965
Qy 440 VVEPNFANKAVCTNGFYSL--HVQSWFGLHKTQ-----APNRLVSDWYNNRLRISM-APPSP 859
Db 966 --EVNLGG-GVPR-HCFEFLMPGTEYKISVHAQLOEIEGPAVSIMETTLPPPTQPTSPS 1021
Qy 473 -----PLVKRVCDTRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLQFVNTLTK 524
Db 1022 TTLPPPTTIPPAKEVCKAAK-----ADLVFLVDGWSIGDDNFNKIISFLYSTVGA 1071
Qy 525 FE-ISTDTRIGAVQVYEQRLBFGPKYSSKPDILNAIKRVGVWSGGTSTGAAINFALE 583
Db 1072 LDKIGDGTQVAILIQSDDPTEFKLNAYKTETLEAIQOIAYKGGNTKGAIKHARE 1131
Qy 584 QLF-----KKSXPNKRKLMILITDGRSYDDVRIPAMAAHLKGVIITVIAIGVAAQAELE 637
Db 1132 VLFTGAGRGKGP---KVLVWITDGRSQDDVNVKVSREMQLDGFSPFAIGVADADYSELV 1188
Qy 638 VIATHPARDSHPVDFEDNLHQVPRILQNIC 669
Db 1189 NIGSKPSERHVFPVDDPDAFTKIEDELITFVC 1220
RESULT 8
S78476
collagen alpha 1(XIV) chain precursor, long form - chicken
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
C;Accession: S78476; S31211
R;Trueb, B.
Submitted to the EMBL Data Library, January 1993
A;Reference number: S78476
A;Accession: S78476
A;Molecule type: mRNA
A;Residues: 1-1888 <TRU>
A;Cross-references: EMBL:X70793; NID:q288872; PIDN:CAA50064.1; PID:q288873
R;Maechli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31211
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416;1460-1811,1843-1888 <WAE>
A;Cross-references: EMBL:X70793
C;Genetics:
A;Gene: Col14A1
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
F;352-433/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;534-614/Domain: fibronectin type III repeat homology <FN3D>
F;623-707/Domain: fibronectin type III repeat homology <FN3E>

F;741-823/Domain: fibronectin type III repeat homology <FN3P>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3H>
F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>
Query Match 9.5%; Score 331; DB 2; Length 1888;
Best Local Similarity 24.8%; Pred. No. 1.4e-13;
Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;
Qy 174 IPGTTAQPVTLMQLLAVTAVATPTTLPRPSPSAASTTSIPRQSVGHRQEMD-----227
Db 713 IVGTTAIPPT-----VTTTTTATTPKPTIAVFR-----GVRNLVIDDETSS 757
Qy 228 ---LWSTATVTSQNR-----PRADPGIQDPGSAAFQKPVGVADSLGLVPKEELS 276
Db 758 LRVVWIDSHNAQQPFTVYLTAKGDRABEAIMVPGRQNTLLQP-----LLPDTYK 809
Qy 277 TQSL-----EPVSLGDPNCKIDLSPIDGSTSIGKRRFRIQKQLADVAQALDIGPAGP 330
Db 810 VTIITPIYADGEGVSAPGKTLPLS-----APNRLVSDWYNNRLRISM-APPSP 859
Qy 331 LAG--VVQYGDN---PATHFNKATHNSRDLKTAIEKIQORGLSNVGRASIVTKNFFS 385
Db 860 TMGYRIVYKSIINVPGA---LFTFVG-DINTIL-----ILNLFSGTETYSVKVPAS 906
Qy 386 KANG---NRSGAPNVVWVDGHPDTKVEASRLAR---ESGINIFITIEGAENKQY 439
Db 907 YSTGFSDALTGVAKTLYLGVNTLDTYQVRMTSLCAQMLHRHATAYRVVIESLVGKKQ- 965
Qy 440 VVEPNFANKAVCTNGFYSL--HVQSWFGLHKTQ-----APNRLVSDWYNNRLRISM-APPSP 859
Db 966 --EVNLGG-GVPR-HCFEFLMPGTEYKISVHAQLOEIEGPAVSIMETTLPPPTQPTSPS 1021
Qy 473 -----PLVKRVCDTRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLQFVNTLTK 524
Db 1022 TTLPPPTTIPPAKEVCKAAK-----ADLVFLVDGWSIGDDNFNKIISFLYSTVGA 1071
Qy 525 FE-ISTDTRIGAVQVYEQRLBFGPKYSSKPDILNAIKRVGVWSGGTSTGAAINFALE 583
Db 1072 LDKIGDGTQVAILIQSDDPTEFKLNAYKTETLEAIQOIAYKGGNTKGAIKHARE 1131
Qy 584 QLF-----KKSXPNKRKLMILITDGRSYDDVRIPAMAAHLKGVIITVIAIGVAAQAELE 637
Db 1132 VLFTGAGRGKGP---KVLVWITDGRSQDDVNVKVSREMQLDGFSPFAIGVADADYSELV 1188
Qy 638 VIATHPARDSHPVDFEDNLHQVPRILQNIC 669
Db 1189 NIGSKPSERHVFPVDDPDAFTKIEDELITFVC 1220
RESULT 9
A54849
collagen alpha 1(VII) chain precursor - human
N;Alternate names: procollagen alpha 1(VII) chain
C;Species: Homo sapiens (man)
C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 15-Sep-2003
C;Accession: A54849; PH0844; S16316; I56328; A30296; I84686
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Utito, J.
J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary sequence of the alpha 1(VI
A;Reference number: A54849; MUID:94327588; PMID:8051117
A;Accession: A54849
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-2944 <CHR>
A;Cross-references: GB:L02870; NID:g987124; PIDN:AAA75438.1; PID:g987125
R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
Biochem. Biophys. Res. Commun. 183, 958-963, 1992
A;Title: Molecular cloning and characterization of type VII collagen cDNA.
A;Reference number: PH0844; MUID:92231902; PMID:1567409
A;Accession: PH0844
A;Molecule type: mRNA
A;Residues: 'EPR', 340-475, 'RALSTASHSTLCNRAWRHPCNRGSHWTRAAACEPCNRPASHRAADAG', 524-528, 'C',

A;Cross-references: DDBJ:D11152; DDBJ:D13694; NID:G453698; PIDN:BA02853.1; PID:G453699
A;Experimental source: keratinocyte
A;Note: The authors translated the codon ACC for residues 394 and 397 as Tyr
R;Parente, M.G.; Chung, L.C.; Rynnaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat
Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A;Reference number: S16316; MUID:91334380; PMID:1871109
A;Accession: S16316
A;Molecule type: mRNA
A;Residues: 815-892, 'E', 894-1439 <PAR>
A;Cross-references: GB:M65158; GB:G49017; NID:G180914; PIDN:AAA96439.1; PID:G180915
A;Experimental source: keratinocyte
R;Gammon, W.R.; Abernathy, M.L.; Padilla, K.M.; Prisyayanh, P.S.; Cook, M.E.; Wright, J.
J. Invest. Dermatol. 99, 691-696, 1992
A;Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot
A;Reference number: 156328; MUID:93107742; PMID:1469284
A;Accession: 156328
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'EPR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A;Cross-references: GB:S51236; NID:G262308; PIDN:AA824637.1; PID:G262309
R;Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E.
J. Biol. Chem. 264, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagen
A;Reference number: A30296; MUID:89139437; PMID:2537292
A;Accession: A30296
A;Molecule type: protein
A;Residues: 'A', 1240-1246, 'G', 1248-1250, 'XE', 1253-1255, 'Q', 1257, 'E', 2032, 'C', 2034-2041,
A;Note: two reported peptides cannot be reliably located
R;Greenpan, D.S.
Hum. Mol. Genet. 2, 273-278, 1993
A;Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
A;Reference number: 148103; MUID:93271985; PMID:8499916
A;Accession: 184686
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 2395-2871, 'S', 2873-2944 <RES>
A;Cross-references: GB:L06862; NID:G388713; PIDN:AAA89196.1; PID:G388714
R;Christiano, A.M.; Rynnaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser sub
A;Reference number: A55255; MUID:94224777; PMID:8170945
A;Contents: annotation
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C;Genetics:
A;Gene: GDB:COL7A1; EBR1; EBD1; EB
A;Cross-references: GDB:128750; OMIM:120120
A;Map position: 3p21.3-3p21.3
A;Note: defects in this gene can result in dominant and recessive dystrophic epidermoly
A;Note: there are 118 introns
C;Complex: type VII collagen is probably a homotrimer
C;Function:
A;Description: structural component of extracellular polymer associated with anchoring
F;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproli
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-2944/Product: collagen alpha 1(VII) chain #status predicted <NC1>
F;17-1253/Domain: amino-terminal nonhelical #status predicted <NC1>
F;36-201/Domain: von Willebrand factor type A repeat homology <VWA1>
F;231-318/Domain: fibronectin type III repeat homology <FN1>
F;327-413/Domain: fibronectin type III repeat homology <FN2>
F;414-502/Domain: fibronectin type III repeat homology <FN3>
F;508-593/Domain: fibronectin type III repeat homology <FN4>
F;598-683/Domain: fibronectin type III repeat homology <FN5>
F;686-771/Domain: fibronectin type III repeat homology <FN6>
F;776-862/Domain: fibronectin type III repeat homology <FN7>
F;864-952/Domain: fibronectin type III repeat homology <FN8>
F;954-1045/Domain: fibronectin type III repeat homology <FN9>
F;1052-1219/Domain: von Willebrand factor type A repeat homology <VWA2>
F;1170-1172/Region: cell attachment (R-G-D) motif
F;1199-1253/Region: cysteine/proline-rich
F;1254-2783/Region: interrupted helical
F;1334-1336/Region: cell attachment (R-G-D) motif

F;2008-2010/Region: cell attachment (R-G-D) motif
F;2553-2555/Region: cell attachment (R-G-D) motif
F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;337,786,1109/Binding site: carboxylate (Asn) (covalent) #status predicted
F;2167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro) #status exper
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Binding site: carboxylate (Lys) (covalent) #status experimental
F;2634,2802,2804/Disulfide bonds: interchain #status predicted
Query Match 9.4%; Score 329.5; DB 2; Length 2944;
Best Local Similarity 35.7%; Pred. No. 3 4e-13;
Matches 80; Conservative 37; Mismatches 88; Indels 19; Gaps 4;
QY 470 TLQPLKRVVC-----DTRLACSKTCLNSADIGFVIDGSSSVGTGNFTVLQ 516
Db 2 TLRLVAALCAGILAEAPRVAQRHRTVCTR--LYAADIVFLDGGSSIGRSNPREVRS 59
QY 517 FVTNLTKEFE--ISDTDTTRIGAVOYTYRQLRFGDKYSSKPDILNAIKRVGWSGTST 574
Db 60 FLEGLVLPFSGAASAGQVRFAVTVQSDPRTFGLDAGSGGDVIRAIRELSTKGNMTR 119
QY 575 CAAINPFALEOLF--KSKSPNKKRKLMLITDGRSYDDVRIPANAAHLKGVIITVAIGVAA 632
Db 120 GAAILHVADHVLPLQARPGVPKVCILLITDGSQDLVDTAQORLKGQGVKLVFAVGIKNAD 179
QY 633 QBELEVIATHPARDHSFPVDFDNLHQVPRIIQNICTEFNSOP 676
Db 180 PEELKRVASQPTSDFFPFVNDPSILRTLPLVSRVCTTAGGVP 223
RESULT 10
A45974
collagen alpha 1(XIV) chain precursor, short form 2 - chicken
N;Alternate names: undulin
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Sep-2003
R;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin
J. Biol. Chem. 268, 12177-12184, 1993
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region
ns,
A;Reference number: A45974; MUID:93280195; PMID:8505337
A;Accession: A45974
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-1747 <GER>
A;Experimental source: embryo skin
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBI:133365)
R;Apte, S.S.
submitted to the EMBL Data Library, March 1992
A;Reference number: S30085
A;Accession: S30085
A;Molecule type: mRNA
A;Residues: 1472-1660 <APT>
A;Cross-references: EMBL:X65122; NID:G62871; PIDN:CAA46238.1; PID:G9938175
R;Trueb, J.; Trueb, B.
Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
A;Accession: S22916
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 286-494, 'O', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 <TRU>
R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsemayer, T.F.; van der Rest, M.; Mayne, R.
Eur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
A;Reference number: S17035; MUID:92037585; PMID:1935930
A;Accession: S17035
A;Molecule type: mRNA
A;Residues: 1472-1659 <GOR1>
A;Accession: S20833

A:Molecule type: protein
A:Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trim
F:40-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F:236-317/Domain: fibronectin type III repeat homology <FN3A>
F:326-409/Domain: fibronectin type III repeat homology <FN3B>
F:418-498/Domain: fibronectin type III repeat homology <FN3C>
F:507-591/Domain: fibronectin type III repeat homology <FN3D>
F:625-707/Domain: fibronectin type III repeat homology <FN3E>
F:716-798/Domain: fibronectin type III repeat homology <FN3F>
F:806-893/Domain: fibronectin type III repeat homology <FN3G>
F:924-1089/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>
F:1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F:1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>

Query Match 9.48; Score 329; DB 2; Length 1747;
Best Local Similarity 24.8; Pred. No. 1.7e-13;
Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

QY 174 IPGTTAQPVTLQMLAVTVAVATPTTLPRPSPSAATTSIPRQSVGHRSEMD----- 227
DB 597 IVGTAPPT-----VTTTTTTTATPKPTIAVFT-----GVRLVIDDETSS 641

QY 228 ---LWSTATTSSNR-----PRADPGIQRQDPGSAAPQKPGVADVSLGLVPKEELS 276
DB 642 LRVVWDISDENAQFRVYTLTAKGDRAEAIMVGRQNTLLQP-----LLPDTYK 693

QY 277 TQSL-----EPVSLGPNCKIDSLFLDCSTSGIKRRFRIOKLLADVAQALDIPAGP 330
DB 694 VTTPPIVADGEGSVSAPGKTLPLS-----APNLRVSDENWRLRISWD-APPSP 743

QY 331 LAG--VVQYGDN---PATHFNKLTHTNSRDLKTAIEKIQTORGSLNVRGSAISFVTKNFFS 385
DB 744 TMGVRIYKSNVPGPA---LETFVGD-DINTIL-----ILNLPSTGYSVKVPAS 790

QY 386 KANG---NRSGAPNVVVMVDGWPDKVBEASRLAR---ESGINIPITIEGAANEKQY 439
DB 791 YSTGFSDALAGVAKTLVGLVNTLDYQVRMTSLCAQQLHRHATRYRWVIESLVGKKQ- 849

QY 440 VVPEPNFANKAVCTNGFVSL--HVQSWFLGHLTKLQ----- 472
DB 850 --EVNLGG-GVPR-HCFELMPGTGYEIKSVHAQLEIGEPASVIMETTLFPPTQPTSPS 905

QY 473 -----PLVPRVCDTDLRLCAKSCNLSADIGFVIGSSSVGTGNFRTVLQVFNLTKE 524
DB 906 TLLPPTPIPAKVCYKAAK-----ADLVFLVDGWSIGDNNFNKLIISFLYSTVGA 955

QY 525 FB-ISDTRIGAVQVYTBORLEFGPKYSSKPDILNAIKRVGWSGTSCTGAANFALE 583
DB 956 LDKIGPDGTVAITQFSDDPRTPEKLNAYKTETLLEAIQOIAYKGGNTKTGKAIRARE 1015

QY 584 QLF-----KSKENKPKMLITDGRSYDDVRIPAMAHLKGVITVIGVAVMAAQEELE 637
DB 1016 VLFTEAGMRGIP---KVLVITDGRSQDDVNKVSREMQLDGFSPFAIGVADADYSELV 1072

QY 638 VIATHPRDHSFFVDEFDNLHQYVPRIONIC 669
DB 1073 NIGSKPSERHVPFVDDFAFTKIEDELITFVC 1104

RESULT 11
T28797
hypothetical protein C16B9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T28797
R:Geisel, C.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C16E9.
A:Reference number: Z20525
A:Accession: T28797
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-567 <GB1>
A:Cross-references: EMBL:U93677; PIDN:AAC47957.1; GSPDB:GN00028; CESP:C16E9.1
A:Experimental source: strain Bristol N2; clone C16E9
C:Genetics:
A:Gene: CESP:C16E9.1
A:Map position: X
A:Introns: 15/3; 77/3; 132/1; 185/3; 231/1; 271/2; 301/2; 430/3; 509/1

Query Match 9.08; Score 314.5; DB 2; Length 567;
Best Local Similarity 22.08; Pred. No. 3e-13;
Matches 130; Conservative 84; Mismatches 213; Indels 163; Gaps 20;

QY 172 PPIPGTTAQPVTLQMLAVTVAVATPTTLPRPSP-SAAATTSIPRQSVGHRSEMDLWS 230
DB 37 PMP-----PTDPPGYDSDFTDTPTTAPPSSNGLRAPPMPKWT 75

QY 231 TATYTSSONRP-----RADPGIQRQDPGSAAPQKPGVADVSLGLVPKEELSTQSL 280
DB 76 QRIPKSSGQOLKIBDVVGNNDISHVEEVNGSGDTEGSGDGKSTESPDASGEA 135

QY 281 EPVSLGD-----PNCKIDLSFLIDGSTSIGKRRFRIOKLLADVAQALDIPG 327
DB 136 QGDSLDPDKMAMDSEAEVLGVNCPDIIIFVIDATSSV-RGIFEQVITYIEKVVEGLDVQP 194

QY 328 AGPLMGVVQYGD---NPATFNKLTHTNSRDLKTAIEKIQTORGSLNVRGSAISFVTKNFFS 385
DB 195 TVDHVGAIVYSSEKKQRTKIKLGEHHDGRGSLVKADELPPFSGITATQALKFAANH--- 251

QY 386 KANGNRSGAPNVVVMVDGWPDKVBEASRLARSEGINIPITIEGAANEKQYVVPNF 445
DB 252 -TEGRRENFTLVYLTIDGYSDILIESGARVLE-----VENS 288

QY 446 ANKAVCRTNGFVSLHVQSWFLGHLTKLQ-----PLVPR--VCDT----- 481
DB 289 A-----IYAVSIGRIP-LRKELEMITGNPNVLTGSMSTGLVVKRLKLCDAIRKAA 338

QY 482 -----DLACS-----KTCLSADIGF 498
DB 339 TLKDSNPLVRPGFLSDRFQHRSLTANLEAKKHEDFVKTPKRGVPKDCI---YDIGI 396

QY 499 VIDGSSSVGTGNFRTVLQVFNLTKEFISDTRIGAVQVYTBORLEFGPKYSSKPDIL 558
DB 397 IPDSSGSL-EKNFQKQALAPAKQLVQMPISDNATRVGIVQAGTKVRLANFSPQKSQL 455

QY 559 LNAIKRVGWSGTSCTGAANFALEQLEPKSK-PNKRKMLILITDGRSYDDVRIPAMAHAH 617
DB 456 KTIIDRSPFYSGTTFITNQALK-KMAALVEESKRPNAKILKMLFTDGYSAEDTSEGEALK 514

QY 618 LKGVITVIGV-----AWAAQSELEVIATHPARDHSFPVDEFDNLHQYVP 662
DB 515 SQGVVVYTVGISTDKSAGLNKKELRGMAT--SSEHYDSSDFADLLKHFP 562

RESULT 12
T46488
hypothetical protein DKFZp434J065.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46488
R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23035
A:Accession: T46488
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-741 <AAA>
A:Cross-references: EMBL:AL137638
A:Experimental source: adult testis; clone DKFZp434J065
C:Genetics:
A>Note: DKFZp434J065.1

Query Match 8.54; Score 298; DB 2; Length 741;

```

Best Local Similarity   29.8%; Pred. No. 5.7e-12;
Matches    68; Conservative    38; Mismatches    88; Indels    34; Gaps    3;

Qy      476 KRVCDDTRLACSKTKCLNSA-----DIGFVIDGSSSVG 507
       ||| : | : | : | : | : | : | : | : | : | : | : | : |
Db      393 KDVCSTHHGCHEHCIVNNGNSYICKSGEFVLAEDGRCKKCTBGPIDLVPVVDGSKSLG 452

Qy      508 TGNFRFTVLQFVNLTWKSPETSDTTRIGAVQYTYEQRLEFGFDKYSKKPDLINAKRVGY 567
       ||| : | : | : | : | : | : | : | : | : | : | : | : |
Db      453 EENFEVVQKFVTGTIDSLTISPKAARVGLLQYSTQVHTTEPTLRNFSAKDMMKKAHMKY 512

Qy      568 WSGGTSTGAALNFALEQLFKK---SKNKRL---MLITDGSRDYDVRIPMAAAHLKV 621
       ||| : | : | : | : | : | : | : | : | : | : | : | : |
Db      513 MGKGSMTGALKEMPFERSFTQGGEARPLSTRVPRRAIIVTDGRAODDVSEWASKAKANGI 572

Qy      622 ITYAIGVAAQAQEBLEVIATHPARDSHFVDDBFNLTGHQYVPRIIQNIC 669
       ||| : | : | : | : | : | : | : | : | : | : | : | : |
Db      573 TMYAVGVGKALEELQBIASEPTNNKLHYAEADFSTMDISEKKLKGGIC 620

RESULT 13
I51027
type XII collagen alpha-1 chain - eastern newt (fragment)
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 15-Sep-2003
C:Accession: I51027
Dev. Biol. 168, 503-513, 1995
R;Wei, Y.; Yang, B.V.; Klatt, K.P.; Tassava, R.A.
A>Title: Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII collagen
A:Reference number: I51027; MUID:95246925; PMID:7729585
A:Accession: I51027
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-929 <WEI>
A:Cross-references: EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g632648
F:155-236/Domain: fibronectin type III repeat homology <3PR>
F:631-795/Domain: von Willebrand factor type A repeat homology <WA3>

Query Match          8.0%; Score 280.5; DB 2; Length 929;
Best Local Similarity 31.0%; Pred. No. 1.2e-10;
Matches    63; Conservative    47; Mismatches    88; Indels    5; Gaps    2;

Qy      470 TLQPLVKRCVCDTRLACSKTKCLNSADIGFVIDGSSSVGTGNFRFTVLQFVNLTKEFEISD 529
       ||| : | : | : | : | : | : | : | : | : | : | : | : |
Db      610 TLRDAPRSPIPSGLDC--TTKAQADVLLVDGWSGISGRPNFKIVRNFIIRVVEVFDIGS 667

Qy      530 TDTTRIGAVQYTYEQRLEPGFDKYSKKPDLINAKRVGYWSGGTSTGAALNFALEQLFKKS 589
       ||| : | : | : | : | : | : | : | : | : | : | : | : |
Db      668 DRVOIAVSQYSQSDPRTSEMQLNTHKTKKSLDMAVANLPYKGGNTNTGSALFXILENNFRPG 727

Qy      590 ---KPNKRKLMIITDGSRDYDVRIPMAAAHLKVITYAIGVAAQAQEBLEVIATHPARD 646
       ||| : | : | : | : | : | : | : | : | : | : | : | : |
Db      728 VGRREKARKAIILITDGSOQDIVASIKRYADEGIELYAVGIKNADENELKEIASPDDEL 787

Qy      647 HSFVFVDFNDLGHQYVPRIIQNIC 669
       ||| : | : | : | : | : | : | : | : | : | : | : | : |
Db      788 YMTNVADFSLITNVNDLTENVC 810

RESULT 14
S42373
hypothetical protein T20G5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S42373
R;Smith, A.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42368
A:Accession: S42373
A:Molecule type: DNA
A:Residues: 1-3051 <SMI>
A:Cross-references: EMBL:Z30423; NID:g458479; PID:g458485
C:Genetics:

```

A; Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1; 1181/1; 1201/2; 1244/1; 1281/1; 1321/1; 1361/1; 1401/1; 1441/1; 1481/1; 1521/1; 1561/1; 1601/1; 1641/1; 1681/1; 1721/1; 1761/1; 1801/1; 1841/1; 1881/1; 1921/1; 1961/1; 2001/1; 2041/1; 2081/1; 2121/1; 2161/1; 2201/1; 2241/1; 2281/1; 2321/1; 2361/1; 2401/1; 2441/1; 2481/1; 2521/1; 2561/1; 2601/1; 2641/1; 2681/1; 2721/1; 2761/1; 2801/1; 2841/1; 2881/1; 2921/1; 2961/1; 3001/1; 3041/1; 3081/1; 3121/1; 3161/1; 3201/1; 3241/1; 3281/1; 3321/1; 3361/1; 3401/1; 3441/1; 3481/1; 3521/1; 3561/1; 3601/1; 3641/1; 3681/1; 3721/1; 3761/1; 3801/1; 3841/1; 3881/1; 3921/1; 3961/1; 4001/1; 4041/1; 4081/1; 4121/1; 4161/1; 4201/1; 4241/1; 4281/1; 4321/1; 4361/1; 4401/1; 4441/1; 4481/1; 4521/1; 4561/1; 4601/1; 4641/1; 4681/1; 4721/1; 4761/1; 4801/1; 4841/1; 4881/1; 4921/1; 4961/1; 5001/1; 5041/1; 5081/1; 5121/1; 5161/1; 5201/1; 5241/1; 5281/1; 5321/1; 5361/1; 5401/1; 5441/1; 5481/1; 5521/1; 5561/1; 5601/1; 5641/1; 5681/1; 5721/1; 5761/1; 5801/1; 5841/1; 5881/1; 5921/1; 5961/1; 6001/1; 6041/1; 6081/1; 6121/1; 6161/1; 6201/1; 6241/1; 6281/1; 6321/1; 6361/1; 6401/1; 6441/1; 6481/1; 6521/1; 6561/1; 6601/1; 6641/1; 6681/1; 6721/1; 6761/1; 6801/1; 6841/1; 6881/1; 6921/1; 6961/1; 7001/1; 7041/1; 7081/1; 7121/1; 7161/1; 7201/1; 7241/1; 7281/1; 7321/1; 7361/1; 7401/1; 7441/1; 7481/1; 7521/1; 7561/1; 7601/1; 7641/1; 7681/1; 7721/1; 7761/1; 7801/1; 7841/1; 7881/1; 7921/1; 7961/1; 8001/1; 8041/1; 8081/1; 8121/1; 8161/1; 8201/1; 8241/1; 8281/1; 8321/1; 8361/1; 8401/1; 8441/1; 8481/1; 8521/1; 8561/1; 8601/1; 8641/1; 8681/1; 8721/1; 8761/1; 8801/1; 8841/1; 8881/1; 8921/1; 8961/1; 9001/1; 9041/1; 9081/1; 9121/1; 9161/1; 9201/1; 9241/1; 9281/1; 9321/1; 9361/1; 9401/1; 9441/1; 9481/1; 9521/1; 9561/1; 9601/1; 9641/1; 9681/1; 9721/1; 9761/1; 9801/1; 9841/1; 9881/1; 9921/1; 9961/1; 10001/1; 10041/1; 10081/1; 10121/1; 10161/1; 10201/1; 10241/1; 10281/1; 10321/1; 10361/1; 10401/1; 10441/1; 10481/1; 10521/1; 10561/1; 10601/1; 10641/1; 10681/1; 10721/1; 10761/1; 10801/1; 10841/1; 10881/1; 10921/1; 10961/1; 11001/1; 11041/1; 11081/1; 11121/1; 11161/1; 11201/1; 11241/1; 11281/1; 11321/1; 11361/1; 11401/1; 11441/1; 11481/1; 11521/1; 11561/1; 11601/1; 11641/1; 11681/1; 11721/1; 11761/1; 11801/1; 11841/1; 11881/1; 11921/1; 11961/1; 12001/1; 12041/1; 12081/1; 12121/1; 12161/1; 12201/1; 12241/1; 12281/1; 12321/1; 12361/1; 12401/1; 12441/1; 12481/1; 12521/1; 12561/1; 12601/1; 12641/1; 12681/1; 12721/1; 12761/1; 12801/1; 12841/1; 12881/1; 12921/1; 12961/1; 13001/1; 13041/1; 13081/1; 13121/1; 13161/1; 13201/1; 13241/1; 13281/1; 13321/1; 13361/1; 13401/1; 13441/1; 13481/1; 13521/1; 13561/1; 13601/1; 13641/1; 13681/1; 13721/1; 13761/1; 13801/1; 13841/1; 13881/1; 13921/1; 13961/1; 14001/1; 14041/1; 14081/1; 14121/1; 14161/1; 14201/1; 14241/1; 14281/1; 14321/1; 14361/1; 14401/1; 14441/1; 14481/1; 14521/1; 14561/1; 14601/1; 14641/1; 14681/1; 14721/1; 14761/1; 14801/1; 14841/1; 14881/1; 14921/1; 14961/1; 15001/1; 15041/1; 15081/1; 15121/1; 15161/1; 15201/1; 15241/1; 15281/1; 15321/1; 15361/1; 15401/1; 15441/1; 15481/1; 15521/1; 15561/1; 15601/1; 15641/1; 15681/1; 15721/1; 15761/1; 15801/1; 15841/1; 15881/1; 15921/1; 15961/1; 16001/1; 16041/1; 16081/1; 16121/1; 16161/1; 16201/1; 16241/1; 16281/1; 16321/1; 16361/1; 16401/1; 16441/1; 16481/1; 16521/1; 16561/1; 16601/1; 16641/1; 16681/1; 16721/1; 16761/1; 16801/1; 16841/1; 16881/1; 16921/1; 16961/1; 17001/1; 17041/1; 17081/1; 17121/1; 17161/1; 17201/1; 17241/1; 17281/1; 17321/1; 17361/1; 17401/1; 17441/1; 17481/1; 17521/1; 17561/1; 17601/1; 17641/1; 17681/1; 17721/1; 17761/1; 17801/1; 17841/1; 17881/1; 17921/1; 17961/1; 18001/1; 18041/1; 18081/1; 18121/1; 18161/1; 18201/1; 18241/1; 18281/1; 18321/1; 18361/1; 18401/1; 18441/1; 18481/1; 18521/1; 18561/1; 18601/1; 18641/1; 18681/1; 18721/1; 18761/1; 18801/1; 18841/1; 18881/1; 18921/1; 18961/1; 19001/1; 19041/1; 19081/1; 19121/1; 19161/1; 19201/1; 19241/1; 19281/1; 19321/1; 19361/1; 19401/1; 19441/1; 19481/1; 19521/1; 19561/1; 19601/1; 19641/1; 19681/1; 19721/1; 19761/1; 19801/1; 19841/1; 19881/1; 19921/1; 19


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Qy 427 ITIEGAENBKOYVVEP-----NFANKAVCRTNGFYSLHVQSWFGLHKTLOPL 474
Db 1399 RYVQGL--KKKKVIVFVGIGPHANLKQIRLIEQAPENKAPVLSVDE--LEQORDEI 1453
Qy 475 VKRVCDDRDLACSKTC-----LNS--ADIGFVIDGSSSVGTGN 510
Db 1454 VSYLCDLAPAPPPTLPHPMAQVTVPGCLLGVSITLGPKNENMVLDAFVLEGSCKIGEAD 1513
Qy 511 FRTVLQFVNTLTKFBISDTRIGAVQYTYEQRLFCGDKYSSKPDILINAIKRVGYWSG 570
Db 1514 FNRSKFPMBEVIQRMVQGDSDIHVTVLQYSYMTVVEYFPEAQSGDILQVRREIRYQGG 1573
Qy 571 G-TSTGRAINFALBQLKCKSKENKK---LMLITDGRSYDDV-RIPAMAHLKGVITTA 625
Db 1574 NRTWTGLALRYLSHSLVSVSQDREQAPNLVYMTGNPASDEIRKLPG-----DIQVVP 1627
Qy 626 IGVAWAAQ-BELEVIATHPARDSFFVDFDNLHGYVPRIIQNIC 669
Db 1628 IGVGNANVQELERIGWPNA---PILIQDFETLPREAPDLVLQRC 1669
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Search completed: May 27, 2004, 16:47:36
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 16:42:02 ; Search time 60 Seconds
(without alignments)
3192.787 Million cell updates/sec

Title: US-10-063-688-34

Perfect score: 3502
Sequence: 1 MRTVLTAKASVIEFLVLL.....QYVPRIIQICTERNQPRN 678

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3502	100.0	678	3	AAy66674	Membrane-
2	3502	100.0	678	4	AAU29098	Human PRO
3	3502	100.0	678	4	AAB87542	Human PRO
4	3502	100.0	678	4	AAB65197	Human PRO
5	3502	100.0	678	5	ABG95867	Human sec
6	3502	100.0	678	6	ABU58474	Human PRO
7	3502	100.0	678	6	ABU88022	Novel hum
8	3502	100.0	678	6	ABU84337	Human sec
9	3502	100.0	678	6	ABR66211	Human sec
10	3502	100.0	678	6	ABR65601	Human sec
11	3502	100.0	678	6	ABU99541	Human sec
12	3502	100.0	678	6	ABU58012	Human PRO
13	3502	100.0	678	6	ABU59090	Novel hum
14	3502	100.0	678	6	ABU82602	Human PRO
15	3502	100.0	678	6	ABU82780	Human PRO
16	3502	100.0	678	6	ABU89901	Novel hum
17	3502	100.0	678	6	ABR68150	Human sec
18	3502	100.0	678	6	ABU60521	Human sec
19	3502	100.0	678	6	ABU96203	Novel hum
20	3502	100.0	678	6	ABU92634	Human sec
21	3502	100.0	678	6	ABO08711	Human sec
22	3502	100.0	678	6	ABO02763	Human sec
23	3502	100.0	678	6	ABR74917	Human sec
24	3502	100.0	678	6	ABR94679	Human sec
25	3502	100.0	678	6	ABU13903	Human PRO

26	3502	100.0	678	6	ABU85652	Human PRO
27	3502	100.0	678	6	ABU98812	Novel hum
28	3502	100.0	678	6	ABU98027	Novel hum
29	3502	100.0	678	6	ABU91733	Novel hum
30	3502	100.0	678	6	ABU89426	Human PRO
31	3502	100.0	678	6	ABU86267	Human sec
32	3502	100.0	678	6	ABU67480	Human sec
33	3502	100.0	678	6	ABU80508	Human PRO
34	3502	100.0	678	6	ABU72488	Novel hum
35	3502	100.0	678	6	ABU90892	Novel hum
36	3502	100.0	678	6	ABO33951	Human sec
37	3502	100.0	678	6	ABR99426	Human sec
38	3502	100.0	678	6	ABR98816	Human sec
39	3502	100.0	678	6	ABO16339	Human sec
40	3502	100.0	678	6	ABR92239	Human sec
41	3502	100.0	678	6	ABO18880	Human sec
42	3502	100.0	678	6	ABR78301	Human sec
43	3502	100.0	678	6	ABU71968	Novel hum
44	3502	100.0	678	6	ABU85037	Novel hum
45	3502	100.0	678	6	ABO00176	Novel hum

ALIGNMENTS

RESULT 1
AAy66674
ID AAY66674 standard; protein; 678 AA.
XX
AC AAY66674;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1277.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW Pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN W09963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088741P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.


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QY 1 MRTVLTAKASVTEMFLVLLVTGVHNSKETAKIKRKPFTVPQINCVDVAGKIIDPEFTV 60
Db 1 MRTVLTAKASVTEMFLVLLVTGVHNSKETAKIKRKPFTVPQINCVDVAGKIIDPEFTV 60
QY 61 KCPAGCQDPKHYVYGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGSGYKGSYSNG 120
Db 61 KCPAGCQDPKHYVYGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGSGYKGSYSNG 120
QY 121 VQSLSLPRWRRESFIVLESKPKGVTTPSLTYSSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
Db 121 VQSLSLPRWRRESFIVLESKPKGVTTPSLTYSSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
QY 181 PVTLMQLLAVTVAVATPTTLPRPSPAASSTTSIPRQSVGHRSGQEMDLNSTATTYSSQNR 240
Db 181 PVTLMQLLAVTVAVATPTTLPRPSPAASSTTSIPRQSVGHRSGQEMDLNSTATTYSSQNR 240
QY 241 PRADPGIQRQDPGSAAPQKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDG 300
Db 241 PRADPGIQRQDPGSAAPQKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDG 300
QY 301 STSIGKRRFRIOQLLADVAQALDIPAGPLMGVVOYGDNPATFNLKTHNSRDLKTAI 360
Db 301 STSIGKRRFRIOQLLADVAQALDIPAGPLMGVVOYGDNPATFNLKTHNSRDLKTAI 360
QY 361 EKITQRGGLSNVGRALISFVTKNPFESKANGRSNAPNVMVWDGWPDKVEASRLARES 420
Db 361 EKITQRGGLSNVGRALISFVTKNPFESKANGRSNAPNVMVWDGWPDKVEASRLARES 420
QY 421 GINIFITIEGAENKQYVVEPNFANKAVCRITNGFVSLHVQSWFGLHKTLOPLVKRCD 480
Db 421 GINIFITIEGAENKQYVVEPNFANKAVCRITNGFVSLHVQSWFGLHKTLOPLVKRCD 480
QY 481 TDRLACSKTCLNSADIGFVIDGSSSVGCTGNFRTVLPQVFNLTKEFRIISDTDRIGAVQYT 540
Db 481 TDRLACSKTCLNSADIGFVIDGSSSVGCTGNFRTVLPQVFNLTKEFRIISDTDRIGAVQYT 540
QY 541 YEORLEFGFDKYSSKPDILNAIKRVGTWSGCTGTGAALNPALEQLFKKSKPKNKKLMILI 600
Db 541 YEORLEFGFDKYSSKPDILNAIKRVGTWSGCTGTGAALNPALEQLFKKSKPKNKKLMILI 600
QY 601 TDCRSYDDVRIIPAAHAKGVITTAIGVAAWAAQEELEVIATHPARDHSPFVDFDNLHQY 660
Db 601 TDCRSYDDVRIIPAAHAKGVITTAIGVAAWAAQEELEVIATHPARDHSPFVDFDNLHQY 660
QY 661 VPRIIQNICTEFNSQPRN 678
Db 661 VPRIIQNICTEFNSQPRN 678

RESULT 3
AAB87542
ID AAB87542 standard; protein; 678 AA.
XX
AC AAB87542;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1277.
XX
KW Human; PRO protein; mapping.
XX
OS Homo sapiens.
XX
PN W0200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000MO-US023328.
XX
PR 01-SEP-1999; 99WO-US020111.
XX
PR 15-SEP-1999; 99WO-US021090.
XX
PR 07-DEC-1999; 99US-0169495P.
XX
PR 09-DEC-1999; 99US-0170262P.
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PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000MO-US0004341.
PR 18-FEB-2000; 2000MO-US0004342.
PR 22-FEB-2000; 2000MO-US0004414.
PR 01-MAR-2000; 2000MO-US0005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000MO-US0008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000MO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
PA (GETH ) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2001-183260/18.
DR N-PSDB; AAF92074.
XX
XX
PT Bighey four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
XX Claim 12; Fig 34; 278pp; English.
XX
XX The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping
XX
XX SQ Sequence 678 AA;
QY Query Match 100.0%; Score 3502; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 8.4e-307;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRTVLTAKASVTEMFLVLLVTGVHNSKETAKIKRKPFTVPQINCVDVAGKIIDPEFTV 60
Db 1 MRTVLTAKASVTEMFLVLLVTGVHNSKETAKIKRKPFTVPQINCVDVAGKIIDPEFTV 60
QY 61 KCPAGCQDPKHYVYGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGSGYKGSYSNG 120
Db 61 KCPAGCQDPKHYVYGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGSGYKGSYSNG 120
QY 121 VQSLSLPRWRRESFIVLESKPKGVTTPSLTYSSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
Db 121 VQSLSLPRWRRESFIVLESKPKGVTTPSLTYSSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
QY 181 PVTLMQLLAVTVAVATPTTLPRPSPAASSTTSIPRQSVGHRSGQEMDLNSTATTYSSQNR 240
Db 181 PVTLMQLLAVTVAVATPTTLPRPSPAASSTTSIPRQSVGHRSGQEMDLNSTATTYSSQNR 240
QY 241 PRADPGIQRQDPGSAAPQKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDG 300
Db 241 PRADPGIQRQDPGSAAPQKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDG 300
QY 301 STSIGKRRFRIOQLLADVAQALDIPAGPLMGVVOYGDNPATFNLKTHNSRDLKTAI 360
Db 301 STSIGKRRFRIOQLLADVAQALDIPAGPLMGVVOYGDNPATFNLKTHNSRDLKTAI 360
QY 361 EKITQRGGLSNVGRALISFVTKNPFESKANGRSNAPNVMVWDGWPDKVEASRLARES 420
Db 361 EKITQRGGLSNVGRALISFVTKNPFESKANGRSNAPNVMVWDGWPDKVEASRLARES 420
QY 421 GINIFITIEGAENKQYVVEPNFANKAVCRITNGFVSLHVQSWFGLHKTLOPLVKRCD 480
Db 421 GINIFITIEGAENKQYVVEPNFANKAVCRITNGFVSLHVQSWFGLHKTLOPLVKRCD 480
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QY 481 TDLRACSKTCLNSADIGFVIDSSVGTGNTFRVLOFVNTLTKFEISDTDTTRIGAVQYT 540
Db 481 TDLRACSKTCLNSADIGFVIDSSVGTGNTFRVLOFVNTLTKFEISDTDTTRIGAVQYT 540
QY 541 YEORLEFGFDKYSSKPDILNAIKRVGYMSGTGTGAALNPALEQLFKKSKPKKRLMILI 600
Db 541 YEORLEFGFDKYSSKPDILNAIKRVGYMSGTGTGAALNPALEQLFKKSKPKKRLMILI 600
QY 601 TGRSYDDVRIPAMAHLKGVITTAIGVAMAAQBELEVIATHPARDHSFFVDFDNLHQY 660
Db 601 TGRSYDDVRIPAMAHLKGVITTAIGVAMAAQBELEVIATHPARDHSFFVDFDNLHQY 660
QY 661 VPRIIQNICTEFNSOPRN 678
Db 661 VPRIIQNICTEFNSOPRN 678

RESULT 4
AAB65197
ID AAB65197 standard; protein; 678 AA.
XX AC
XX AAB65197;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1277 (UNQ647) protein sequence SEQ ID NO:179.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 28-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 12-FEB-2000; 2000WO-US004341.
PR 28-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
XX (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy WA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.

N-PSDB; AAF44155.
PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
Claim 12; Fig 113; 935pp; English.
The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
XX Sequence 678 AA;
SQ

Query Match 100.0%; Score 3502; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 8.4e-307;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRTVLTWKASVIEMLVLLVTVGHSNKRKTAKKIKRPKFTVPQINCDCVAGKIIIDPEFTV 60
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QY 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPSQVGHRSQBDMLNSTATYTSQNR 240
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QY 241 PRADPGIQRQDPSCGAAFQKPVGADVSLGLVPKBEISTQSLEPVSIGDPNCKIDLSFLIDG 300
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QY 361 EKITQRGSLNVRGAI SFVTKNPFESKANGNSGAPNVMVVDGWPTDKVBSRLARES 420
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QY 601 TGRSYDDVRIPAMAHLKGVITTAIGVAMAAQBELEVIATHPARDHSFFVDFDNLHQY 660
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OY 661 VPRIIQUICTEFSQPRN 678
 DB 661 VPRIIQUICTEFSQPRN 678

RESULT 5

ABG95867
 ID ABG95867 standard; protein; 678 AA.

AC ABG95867;
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DT 10-DEC-2002 (first entry)
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DE Human secreted/transmembrane protein PRO1277.
 XX

KW Human; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

OS Homo sapiens.
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XX US2002119130-A1.
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XX 29-AUG-2002.
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PF 06-DEC-2001; 2001US-00006867.
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PR 29-OCT-1997; 97US-0063435P.
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PR 29-OCT-1997; 97US-0064215P.
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PR 22-APR-1998; 98US-0082797P.
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PR 16-SEP-1

CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention
XX
SQ

Sequence 678 AA;

Query Match 100.0%; Score 3502; DB 5; Length 678;
Best Local Similarity 100.0%; Pred. No. 8.4e-307;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLTLTKASVIEMLFLLVLTGSHNKEETAKIKRPFTVPQINCDVKAGKIIDPEFIV 60
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Qy 61 KCPAGCQDPKTHVGTDTVYASVSYCGAAVHSGVLDNSGGKILVRKVGQSGYKGSYNG 120
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Qy 121 VQSLSLRWRRESFVLESKPKKGVTPSALYSSSKSPAAOAGETTKAYQRPPIGTTAQ 180
Db 121 VQSLSLRWRRESFVLESKPKKGVTPSALYSSSKSPAAOAGETTKAYQRPPIGTTAQ 180

Qy 181 PVTLMLLAVTVAVATPTLPRPSPASATTSIPRQSVGHRSGMDLWSTATTYSSQNR 240
Db 181 PVTLMLLAVTVAVATPTLPRPSPASATTSIPRQSVGHRSGMDLWSTATTYSSQNR 240

Qy 241 PRADPGIQRQDPGSAAPQKPGVADVSLGVPKEBELSTQSLPVSGLDPNCKIDLSFLIDG 300
Db 241 PRADPGIQRQDPGSAAPQKPGVADVSLGVPKEBELSTQSLPVSGLDPNCKIDLSFLIDG 300

Qy 301 STSIGKRFRIOKQLADVAQALDIGPAGPLMGVYQYGDNPATHPNLKHTNSRDLKTAI 360
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Qy 361 EKI TORGLSNVGRASIFVTKNPFSGKANGNSGAPNVMVDGWPDTKVBEASRLARES 420
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Qy 601 TDGRSYDDVRIPAMAHLKGVITYAIGVAAQAEELEVIATHPARDHSPFVDFDNLHGY 660
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Qy 661 VPIIIONICTEFSQPRN 678
Db 661 VPIIIONICTEFSQPRN 678

RESULT 6

ABU58474

ID ABU58474 standard; protein; 678 AA.

XX AC ABU58474;
XX DT 15-APR-2003 (first entry)
XX DE Human PRO polypeptide #75.
XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
XX KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
XX KW antibody-dependent enzyme mediated prodrug therapy.
XX OS Homo sapiens.
XX PN US2003027272-A1.
XX PD 06-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176492.
XX PR 18-SEP-1997; 97US-0059263P.
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PR 17-OCT-1997; 97US-0062250P.
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PR 28-OCT-1997; 97US-0063540P.
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PR	16-JUN-1998;	98US-0089514P.	PR	23-SEP-1998;	98US-0101472P.
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PR	22-JUN-1998;	98US-0090246P.	PR	24-SEP-1998;	98US-0101922P.
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PR	24-JUN-1998;	98US-0090435P.	PR	29-SEP-1998;	98US-0102240P.
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PR	25-JUN-1998;	98US-0090688P.	PR	01-OCT-1998;	98US-0102687P.
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Db	1	MRTVLTWQASVIEMLVLLVTVGHSNKTAKKIKRPKFTVPQINCVDVKGAKIIDPPIV	60	1	MRTVLTWQASVIEMLVLLVTVGHSNKTAKKIKRPKFTVPQINCVDVKGAKIIDPPIV
Qy	61	KCPAGCQDPKHYVTGTDVYASVSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG	120	61	KCPAGCQDPKHYVTGTDVYASVSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG
Db	61	KCPAGCQDPKHYVTGTDVYASVSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG	120	61	KCPAGCQDPKHYVTGTDVYASVSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG
Qy	121	VQSLSPRWRESFIVLESKPKKGVTPYPSALTYSSKSPAAQAGETTKAYQRPPIGTTAQ	180	121	VQSLSPRWRESFIVLESKPKKGVTPYPSALTYSSKSPAAQAGETTKAYQRPPIGTTAQ
Db	121	VQSLSPRWRESFIVLESKPKKGVTPYPSALTYSSKSPAAQAGETTKAYQRPPIGTTAQ	180	121	VQSLSPRWRESFIVLESKPKKGVTPYPSALTYSSKSPAAQAGETTKAYQRPPIGTTAQ
Qy	181	PVTLQMLLVAVATPTTLPRPSPSAASTTTSIPRPSQVGHRSQEMDLWSTATYTTSSQNR	240	181	PVTLQMLLVAVATPTTLPRPSPSAASTTTSIPRPSQVGHRSQEMDLWSTATYTTSSQNR
Db	181	PVTLQMLLVAVATPTTLPRPSPSAASTTTSIPRPSQVGHRSQEMDLWSTATYTTSSQNR	240	181	PVTLQMLLVAVATPTTLPRPSPSAASTTTSIPRPSQVGHRSQEMDLWSTATYTTSSQNR

Query Match 100.0%; Score 3502; DB 6; Length 678;

Best Local Similarity 100.0%; Pred. No. 8.4e-307; Mismatches 0; Indels 0; Gaps 0;

Matches 678; Conservative 0;

Qy	241	PRADPGIQORPPSGAARFQKPGADVSLGLVPKEBLSTOSLEPVSIGDPNCKIDLSFLIDG	300	PR	24-NOV-1997;	97US-0066466P.
Db	241			PR	24-NOV-1997;	97US-0066772P.
Qy	301	STSIKGRFRIOKOLLADVAQALDIPGAGPLMGVVOYGDNEPATHFNLTHTNSRDLKTAI	360	PR	12-DEC-1997;	97US-0069435P.
Db	301			PR	12-DEC-1997;	97US-0069870P.
Qy	361	EKITORGCLSNVGRASISFVTNKFSSKANGNSGAPNVVVMDGMPDKVEEASRLARES	420	PR	18-DEC-1997;	97US-0068017P.
Db	361			PR	10-MAR-1998;	98US-0077450P.
Qy	421	GINIFFITIEGAENBKQYVVEPNFAKAVCRITNGFTSLVQSWFGLHKTLOPLVKRVCD	480	PR	11-MAR-1998;	98US-0077632P.
Db	421			PR	11-MAR-1998;	98US-0077649P.
Qy	481	TDLRACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKPEISDTRIGAVOYT	540	PR	20-MAR-1998;	98US-0078939P.
Db	481			PR	27-MAR-1998;	98US-0079664P.
Qy	541	YEORLEFGFDKYSKPDILNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPKRKLMLLI	600	PR	27-MAR-1998;	98US-0079786P.
Db	541			PR	31-MAR-1998;	98US-0080107P.
Qy	601	TGGRSYDDVRIPMAAHLKGVITTAIGVAAQAQBELEVIATHPARDHSFFVDFDNLHQY	660	PR	01-APR-1998;	98US-0080327P.
Db	601			PR	08-APR-1998;	98US-0081049P.
Qy	661	VPRIIIONICTEFNSQPRN 678		PR	09-APR-1998;	98US-0081155P.
Db	661			PR	15-APR-1998;	98US-0081838P.
RESULT 7				PR	21-APR-1998;	98US-0082568P.
ABU88022				PR	22-APR-1998;	98US-0082704P.
ID	ABU88022	standard; protein; 678 AA.		PR	22-APR-1998;	98US-0082797P.
AC	ABU88022;			PR	28-APR-1998;	98US-0083322P.
DT	07-JUL-2003 (first entry)			PR	29-APR-1998;	98US-0083495P.
DE	Novel human secreted and transmembrane protein PRO1277.			PR	29-APR-1998;	98US-0083496P.
KW	Human; secreted and transmembrane protein: PRO; gene therapy;			PR	29-APR-1998;	98US-0083499P.
KW	tumour necrosis factor-alpha release; TNF-alpha release;			PR	29-APR-1998;	98US-0083559P.
KW	chondrocyte proliferation; chondrocyte differentiation; tumour;			PR	05-MAY-1998;	98US-0084366P.
KW	adrenal tumour; lung tumour; colon tumour; breast tumour;			PR	06-MAY-1998;	98US-0084414P.
KW	prostate tumour; rectal tumour; cervical tumour; liver tumour.			PR	07-MAY-1998;	98US-0084639P.
XX	Homo sapiens.			PR	07-MAY-1998;	98US-0084640P.
XX	US2003032127-A1.			PR	15-MAY-1998;	98US-0085579P.
XX	13-FEB-2003.			PR	15-MAY-1998;	98US-0085580P.
XX	26-JUN-2002; 2002US-00183012.			PR	15-MAY-1998;	98US-0085582P.
PR	18-SEP-1997; 97US-0059263P.			PR	18-MAY-1998;	98US-0086023P.
PR	18-SEP-1997; 97US-0059266P.			PR	22-MAY-1998;	98US-0086392P.
PR	17-OCT-1997; 97US-0062250P.			PR	28-MAY-1998;	98US-0086486P.
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PR	28-OCT-1997; 97US-0063540P.			PR	02-JUN-1998;	98US-0087609P.
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PR	28-OCT-1997; 97US-0063564P.			PR	04-JUN-1998;	98US-0088025P.
PR	29-OCT-1997; 97US-0063734P.			PR	04-JUN-1998;	98US-0088028P.
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Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 8,4e-307;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRTVLTMTKASVIEMFLVLLVTGVHSHKETAAXIKRPKFTVPQINCVDVKAGKIIDPFIY 60

Qy 61 KCPAGCQDPKYHYGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGSGYKGSYNG 120
Db 61 KCPAGCQDPKYHYGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGSGYKGSYNG 120

Qy 121 VQSLSLPRWRRESFIVLESKPKKGVTPYSALTYSSSSPAAQAGETTKAYORPPIPGTTAQ 180
Db 121 VQSLSLPRWRRESFIVLESKPKKGVTPYSALTYSSSSPAAQAGETTKAYORPPIPGTTAQ 180

Qy 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRQSVGRHRSQEMDLMTATYTSSQNR 240
Db 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRQSVGRHRSQEMDLMTATYTSSQNR 240

Qy 241 PRADPGIQRQDPGSAAPQKPVGADVSLGLVPKBEELSTQSLPEVSLGDPNCKIDLSFLIDG 300
Db 241 PRADPGIQRQDPGSAAPQKPVGADVSLGLVPKBEELSTQSLPEVSLGDPNCKIDLSFLIDG 300

Qy 301 STSIGKRRFRIQKQLLADVAQAOLDIGPAGPLMGVVOYGDNPATHEMLKHTNSRDLKTAI 360
Db 301 STSIGKRRFRIQKQLLADVAQAOLDIGPAGPLMGVVOYGDNPATHEMLKHTNSRDLKTAI 360

Qy 361 EKITORGGLSNVGRALSFVTKNFFSKANGNRSGAPNVVVVMDGMPDVKVEEASRLARES 420
Db 361 EKITORGGLSNVGRALSFVTKNFFSKANGNRSGAPNVVVVMDGMPDVKVEEASRLARES 420

Qy 421 GINIFPITIEGAANEKQYVVEPNFANKAVCRTNGFPYSLHVQSWFGLHKTLOPLVKRVCV 480
Db 421 GINIFPITIEGAANEKQYVVEPNFANKAVCRTNGFPYSLHVQSWFGLHKTLOPLVKRVCV 480

Qy 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVLOFVTVNLTKPEFISDTRIGAVOYT 540
Db 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVLOFVTVNLTKPEFISDTRIGAVOYT 540

Qy 541 YEORLEFGFDKYSSKPDILNALKRVGYWSGCTGTGAALNFPALBQLPKKSPKPKKMLILI 600
Db 541 YEORLEFGFDKYSSKPDILNALKRVGYWSGCTGTGAALNFPALBQLPKKSPKPKKMLILI 600

Qy 601 TDCRSYDDVRIIPAMAAHLKGVITYAIGVAAAOEELEVIATHPHARDHSFFVDFDNLHOY 660
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Qy 661 VPRIIQNICTEFNSQPRN 678
Db 661 VPRIIQNICTEFNSQPRN 678

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ABU84337
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ID	ABU84337 standard; protein; 678 AA.	PR	15-MAY-1998;	98US-0085700P.
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XX	ABU84337;	PR	22-MAY-1998;	98US-0086392P.
XX	DT	PR	28-MAY-1998;	98US-0086486P.
XX	02-AUG-2003 (first entry)	PR	28-MAY-1998;	98US-0087098P.
XX	Human secreted/transmembrane protein (PRO) #75.	PR	02-JUN-1998;	98US-0087208P.
XX	DE	PR	02-JUN-1998;	98US-0087603P.
XX	Human; secreted and transmembrane protein; PRO; TNF-alpha;	PR	02-JUN-1998;	98US-0087753P.
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;	PR	03-JUN-1998;	98US-0087827P.
KW	tissue typing.	PR	04-JUN-1998;	98US-0088025P.
XX	OS	PR	04-JUN-1998;	98US-0088028P.
XX	Homo sapiens.	PR	04-JUN-1998;	98US-0088029P.
XX	US2003032112-A1.	PR	04-JUN-1998;	98US-0088033P.
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XX	21-JUN-2002; 2002US-00176756.	PR	05-JUN-1998;	98US-0088167P.
XX	18-SEP-1997; 97US-0059263P.	PR	05-JUN-1998;	98US-0088202P.
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Mismatches

Conservative

Mismatches

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Qy	301	STSIGKRRFRIQKOLLADVAQALDIPAGPLMGVVQYGDNPATFNLTHTNSRDLKTAI	360	PR	12-DEC-1997;	97US-0069425P.
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AC ABUS8012;
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DT 14-APR-2003 (first entry)
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KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEFT;
KW antibody-dependent enzyme mediated prodrug therapy.
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OS Homo sapiens.
XX
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PP 15-NOV-2001; 2001US-00997666.
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PR	08-MAR-1999;	99WO-US000528.
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PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US003565.
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PR	24-FEB-2000;	2000WO-US004914;
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PR	09-JUL-2001;	2001WO-US021735
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PR	02-SEP-2001;	2001US-00041992

(GETH) GENENTECH INC.

AA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Geritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kljavin TJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;

WPI; 2003-247083/
N-PSDB: ABX80239.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments.

Claim 12: Fig 113: 648pp: English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO535, PRO943, PRO838, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of infants, e.g. retinitis pigmentosa, AMD. PRO819, PRO813 and PRO11066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein

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Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OM protein - protein search, using sw model

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Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3502	100.0	678	4	Q9UDN0	Q9udn0 homo sapien
2	3484.5	99.5	693	4	Q96DM8	Q96dm8 homo sapien
3	3344	95.5	656	4	Q96DT1	Q96dt1 homo sapien
4	2823	80.6	650	11	Q8VHT5	Q8vht5 mus musculus
5	2818	80.5	652	6	Q9SLI2	Q9sl12 bos taurus
6	2801	80.0	650	11	Q8K047	Q8k047 mus musculus
7	2796	79.8	650	11	Q9CYZ1	Q9cyz1 mus musculus
8	2682	76.6	628	11	Q8BQ41	Q8bq41 mus musculus
9	1187.5	33.9	553	13	Q8AW56	Q8aw56 brachydanio
10	1017.5	29.1	494	4	Q96IU6	Q96iu6 homo sapien
11	512	14.6	490	13	Q7SYT5	Q7syrt5 xenopus lae
12	493	14.1	500	11	Q80VNS	Q80vns mus musculus
13	485	13.8	507	13	Q7ZVP3	Q7zvp3 brachydanio
14	463	13.2	1182	11	Q8C6K9	Q8c6k9 mus musculus
15	447.5	12.8	540	4	Q8N2M5	Q8n2m5 homo sapien
16	435.5	12.4	1703	11	Q9Z019	Q9z019 mus musculus

17	409	11.7	488	4	Q8N2M7	Q8n2m7 homo sapien
18	378	10.8	2657	11	Q88493	Q88493 mus musculus
19	360	10.3	1016	4	Q8NDE6	Q8nde6 homo sapien
20	357.5	10.2	937	4	Q96FT5	Q96ft5 homo sapien
21	350.5	10.0	1797	11	Q80X19	Q80x19 mus musculus
22	339.5	9.7	956	11	Q99K64	Q99k64 mus musculus
23	337.5	9.6	956	11	Q8R542	Q8r542 mus musculus
24	334	9.5	721	11	Q8CE01	Q8ce01 mus musculus
25	326	9.3	1253	6	Q97566	Q97566 canis famil
26	326	9.3	2936	6	Q7YRK8	Q7yrk8 canis famil
27	324	9.3	2944	11	Q63870	Q63870 mus musculus
28	323	9.2	517	4	Q43853	Q43853 homo sapien
29	314.5	9.0	567	5	Q18048	Q18048 caenorhabdi
30	313	8.9	453	5	Q8T5C2	Q8t5c2 mytilus gal
31	307	8.8	444	5	Q8T5C3	Q8t5c3 mytilus edu
32	300	8.6	441	5	Q8T6U5	Q8t6u5 mytilus edu
33	300	8.6	755	4	Q00261	Q00261 homo sapien
34	298	8.5	537	4	Q96AA0	Q96aa0 homo sapien
35	298	8.5	715	4	Q7Z5X1	Q7z5x1 homo sapien
36	290.5	8.3	954	4	Q8WV8	Q8wv8 homo sapien
37	290.5	8.3	957	4	Q9H0V3	Q9h0v3 homo sapien
38	290.5	8.3	957	4	Q96P44	Q96p44 homo sapien
39	289.5	8.3	1626	4	Q8NFW1	Q8nfw1 homo sapien
40	282.5	8.1	2813	11	Q8C1Z8	Q8c1z8 mus musculus
41	281	8.0	1472	13	Q90ZAO	Q90za0 gallus gall
42	279	8.0	2104	5	Q964N4	Q964n4 caenorhabdi
43	279	8.0	2104	5	Q21281	Q21281 caenorhabdi
44	271.5	7.8	419	6	Q97925	Q97925 macropus gi
45	271	7.7	549	6	Q02808	Q02808 bos taurus

ALIGNMENTS

RESULT 1

ID	Q9UDN0	PRELIMINARY;	PRT;	678 AA.
AC	Q9UDN0;			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)			
DE	Similar to Coch-5B2.			
GN	WUGSC:H NH0294L11.1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99063792; PubMed=9847074;			
RA	Suleston J.E., Waterston R.;			
RT	"Toward a complete human genome sequence.";			
RL	Genome Res. 8:1097-1108(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Corde M., Kalicki J., Ames M.;			
RT	"The sequence of Homo sapiens BAC clone Rp11-294L11.";			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Waterston R.;			
RT	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AC007363; AAF19243.1; -.			
DR	HSSP; P11215; 1JLM.			
DR	InterPro; IPR004043; ICCL dom.			
DR	InterPro; IPR002035; VWF_A.			
DR	Pfam; PF03815; LCCL; 1.			
DR	Pfam; PF00092; vwa; 2.			
DR	PRINTS; PR00453; VWFADOMAIN.			
DR	SMART; SM00603; LCCL; 1.			
DR	SMART; SM00327; VWA; 2.			
DR	PROSITE; PS50820; LCCL; 1.			
DR	PROSITE; PS50234; VWFA; 2.			

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SQ SEQUENCE 678 AA; 73930 MW; 9870E75A218C686C CRC64;
Query Match 100.0%; Score 3502; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.3e-242; Indels 0; Gaps 0;
Matches 678; Conservative 0; Mismatches 0;

QY 1 MRTVLTMTKASVIEMLVLLVTVGVHNSKETAKKIKRPKFTVPQINCDVKAGKIIDPEPIV 60
DB 1 MRTVLTMTKASVIEMLVLLVTVGVHNSKETAKKIKRPKFTVPQINCDVKAGKIIDPEPIV 60

QY 61 KCPAGCQDPKHYVGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVGSGYKGSYNG 120
DB 61 KCPAGCQDPKHYVGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVGSGYKGSYNG 120

QY 121 VQSLSLPRRRESFVLESPPKGGVTVPSALTYSSSKSPAAQAGETTKAYORPPIPGTTAQ 180
DB 121 VQSLSLPRRRESFVLESPPKGGVTVPSALTYSSSKSPAAQAGETTKAYORPPIPGTTAQ 180

QY 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRQSVGHRSGQEMDLWSTATYTSSQNR 240
DB 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRQSVGHRSGQEMDLWSTATYTSSQNR 240

QY 241 PRADPGIQORDPSGAAPQKPVGADVSLGLVPKEELSTQSLPVSIGDPNCKIDLSELDG 300
DB 241 PRADPGIQORDPSGAAPQKPVGADVSLGLVPKEELSTQSLPVSIGDPNCKIDLSELDG 300

QY 301 STSISGRRFRIOKLLADVAQALDIGPAGPLMGVQYGDNPATFNKLTHTNSRDLKTAI 360
DB 301 STSISGRRFRIOKLLADVAQALDIGPAGPLMGVQYGDNPATFNKLTHTNSRDLKTAI 360

QY 361 EKITQGGLSNVGRAISFVTKNPFPSKANGRSGAPNVVWVDGWPTDKVBEASRLARES 420
DB 361 EKITQGGLSNVGRAISFVTKNPFPSKANGRSGAPNVVWVDGWPTDKVBEASRLARES 420

QY 421 GINIPIITIEGAENKQYVVEPNPANKAVCRNNGFYSLFVQSWPGLHKTLOPLVKRVC 480
DB 421 GINIPIITIEGAENKQYVVEPNPANKAVCRNNGFYSLFVQSWPGLHKTLOPLVKRVC 480

QY 481 TDRLACKTKLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKFEISDTRIGAVQTT 540
DB 481 TDRLACKTKLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKFEISDTRIGAVQTT 540

QY 541 YEORLEFGDKYSSKPDILNAIKRVGWSGGTSTGAAINPALEQLFKSKPNKRKLMILI 600
DB 541 YEORLEFGDKYSSKPDILNAIKRVGWSGGTSTGAAINPALEQLFKSKPNKRKLMILI 600

QY 601 TGRSYDDVRIIPAMAHLKGVITYAIGVANAQSELEVIATHPARHSPFVDFDNLHGY 660
DB 601 TGRSYDDVRIIPAMAHLKGVITYAIGVANAQSELEVIATHPARHSPFVDFDNLHGY 660

QY 661 VPRIIQNICTEFNSQPRN 678
DB 661 VPRIIQNICTEFNSQPRN 678
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RESULT 2

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Q96DM8 PRELIMINARY; PRT; 693 AA.
AC Q96DM8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ32210.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
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RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Mateuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Negahari K., Masuho Y., Negai K., Isogai T.,
RT "NEBO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK056772; BAB71279.1; -.
DR Genew; HGNC:112697; VIT.
DR InterPro; IPR004043; LCCL dom.
DR InterPro; IPR002035; WFP_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; WVFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; WFA; 2.
DR Hypothetical protein.
KW SEQUENCE 693 AA; 75575 MW; 2DE8B2421F2D496D CRC64;
Query Match 99.5%; Score 3484.5; DB 4; Length 693;
Best Local Similarity 97.8%; Pred. No. 2.4e-241; Indels 15; Gaps 1;
Matches 678; Conservative 0; Mismatches 0;

QY 1 MRTVLTMTKASVIEMLVLLVTVGVHNSKETAKKIKRPKFTVPQINCDVKAGKIIDPEPIV 60
DB 1 MRTVLTMTKASVIEMLVLLVTVGVHNSKETAKKIKRPKFTVPQINCDVKAGKIIDPEPIV 60

QY 61 KCPAGCQDPKHYVGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVGSGYKGSYNG 120
DB 61 KCPAGCQDPKHYVGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVGSGYKGSYNG 120

QY 121 VQSLSLPRRRESFVLESPPKGGVTVPSALTYSSSKSPAAQAGETTKAYORPPIPGTTAQ 180
DB 121 VQSLSLPRRRESFVLESPPKGGVTVPSALTYSSSKSPAAQAGETTKAYORPPIPGTTAQ 180

QY 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRQSVGHRSGQEMDLWSTATYTSSQNR 240
DB 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRQSVGHRSGQEMDLWSTATYTSSQNR 240

QY 241 PRADPGIQORDPSGAAPQKPVGADVSLGLVPKEELSTQSLPVSIGDPNCKIDLSELDG 285
DB 241 PRADPGIQORDPSGAAPQKPVGADVSLGLVPKEELSTQSLPVSIGDPNCKIDLSELDG 300

QY 286 GPNCKIDLSFLIDGSTSIGKRRFRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATHP 345
DB 286 GPNCKIDLSFLIDGSTSIGKRRFRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATHP 360

QY 301 GPNCKIDLSFLIDGSTSIGKRRFRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATHP 360
DB 301 GPNCKIDLSFLIDGSTSIGKRRFRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATHP 405

QY 346 NLKHTNSRDLKTAIEKITQGGLSNVGRAISFVTKNPFPSKANGRSGAPNVVWVDGW 420
DB 346 NLKHTNSRDLKTAIEKITQGGLSNVGRAISFVTKNPFPSKANGRSGAPNVVWVDGW 465

QY 406 PTDKVEASRLARESINIFPITIEGAENKQYVVEPNPANKAVCRNNGFYSLHVSQSWP 465
DB 421 PTDKVEASRLARESINIFPITIEGAENKQYVVEPNPANKAVCRNNGFYSLHVSQSWP 480

QY 466 GLHKTLOPLVKRVCDDTLRACSKTKLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKBP 525
DB 481 GLHKTLOPLVKRVCDDTLRACSKTKLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKBP 540

QY 526 EISDTRIGAVQYTYEORLEFGDKYSSKPDILNAIKRVGWSGGTSTGAAINPALEQL 585
DB 541 EISDTRIGAVQYTYEORLEFGDKYSSKPDILNAIKRVGWSGGTSTGAAINPALEQL 600

QY 586 FKSKPNKRKLMILTGRSYDDVRIIPAMAHLKGVITYAIGVANAQSELEVIATHPAR 645
DB 601 FKSKPNKRKLMILTGRSYDDVRIIPAMAHLKGVITYAIGVANAQSELEVIATHPAR 660

QY 646 DHSFFVDFDNLHGYVPRIIQNICTEFNSQPRN 678
DB 661 DHSFFVDFDNLHGYVPRIIQNICTEFNSQPRN 693
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RESULT 3
Q96DT1 PRELIMINARY; PRT; 656 AA.
AC Q96DT1 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vitrin.
GN VIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle, and Fetal heart;
RA Ren Z.-X., Liu J.G., Mayne R.;
RT "Human vitrin complete cDNA sequence.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF063833; AAL18263.1; -.
DR InterPro; IPR004043; LCCL.dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWFA; 2.
SQ SEQUENCE 656 AA; 71767 MW; E242B00DFB07CF2C CRC64;

Query Match 95.5%; Score 3344; DB 4; Length 656;
Best Local Similarity 96.08; Pred. No. 2.7e-231;
Matches 651; Conservative 1; Mismatches 4; Indels 22; Gaps 1;

Qy 1 MRTLVTMKASVIEMLVLLVTGVHSHKETAACKIKRPKFTVPQINCDVKAGKIIDPEFIV 60
Db 1 MRTLVTMKASVIEMLVLLVTGVHSHKETAACKIKRPKFTVPQINCDVKAGKIIDPEFIV 60

Qy 61 KCPAGCQDPKHYVGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVGQSGYKGSYNG 120
Db 61 KCPAGCQDPKHYVGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVGQSGYKGSYNG 120

Qy 121 VQSLSPRRESFVLESKPKGKGYTPSALTYSKSPAAQAGETTKAYQRPPIGTTAQ 180
Db 121 VQSLSPRRESFVLESKPKGKGYTPSALTYSKSPAAQAGETTKAYQRPPIGTTAQ 180

Qy 181 PVTLQMLAVTVAVATPTTLPRPSPAASVTSIIPRQSVGHSQEMDLKSTATTYSSQNR 240
Db 181 PVTLQMLAVTVAVATPTTLPRPSPAASVTSIIPRQSVGHSQEMDLKSTATTYSSQNR 240

Qy 241 PRADPGIQRQDPGSAAPQKPGVADVSLGLVPKBELSTQSLPEVSLGDPNCKIDLSFLIDG 300
Db 241 PRADP-----GLVPKBELSTQSLPEVSLGDPNCKIDLSFLIDG 278

Qy 301 STSIGKRRFRIQKOLLADVAQALDIPAGPLMGVYQVQYGDNPATFNKLTHTNSRDLKTAI 360
Db 279 STSIGKRRFRIQKOLLADVAQALDIPAGPLMGVYQVQYGDNPATFNKLTHTNSRDLKTAI 338

Qy 361 EKIQORGLSNVGRRAISFVTKNFFSKANGNRSGAPNVVVVMDGWPDKVBEASRLARES 420
Db 339 EKIQORGLSNVGRRTISFVTKNFFSKANGNRSGAPNVVVVMDGWPDKVBEASRLARVS 398

Qy 421 GINIFFITTEGAARENEKYVVEPNFANKAVCRITNGFTSLHVQSWFGLHKLQPLVKRVCV 480
Db 399 GINIFFITTEGAARENEKYVVEPNFANKAVCRITNGFTSLHVQSWFGLHKLQPLVKRVCV 458

Qy 481 TDLRACSKTCLNSADIGFVLDGSSSVGTGNFRTVLQFVNTLTKFBISTDTRIGAVQYT 540
Db 459 TDLRACSKTCLNSADIGFVLDGSSSVGTGNFRTVLQFVNTLTKFBISTDTRIGAVQYT 518

Qy 541 YEORLEFGFDKYSKPDILNAIKRVGWSGGTSTGTAAINFALEQLFKKSKPNKKKLMILI 600
Db 541 YEORLEFGFDKYSKPDILNAIKRVGWSGGTSTGTAAINFALEQLFKKSKPNKKKLMILI 600

RESULT 4
Q8VHI5 PRELIMINARY; PRT; 650 AA.
AC Q8VHI5 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vitrin.
GN VIT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Liu J., Ren Z.-X., Takanosu M., Mayne R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF454755; AAL57848.1; -.
DR InterPro; IPR004043; LCCL.dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWFA; 2.
SQ SEQUENCE 650 AA; 70705 MW; FAC0F72APB953940 CRC64;

Query Match 80.6%; Score 2823; DB 11; Length 650;
Best Local Similarity 81.2%; Pred. No. 6.6e-194;
Matches 553; Conservative 36; Mismatches 59; Indels 34; Gaps 5;

Qy 1 MRTLVTMKASVIEMLVLLVTGVHSHKETAACKIKRPKFTVPQINCDVKAGKIIDPEFIV 60
Db 1 MRTLVTMKASVIEMLVLLVTGVHSHKETAACKIKRPKFTVPQINCDVKAGKIIDPEFIV 60

Qy 61 KCPAGCQDPKHYVGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVGQSGYKGSYNG 120
Db 61 KCPAGCQDPKHYVGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVGQSGYKGSYNG 120

Qy 121 VQSLSPRRESFVLESKPKGKGYTPSALTYSKSPAAQAGETTKAYQRPPIGTTAQ 180
Db 121 VQSLSPRRESFVLESKPKGKGYTPSALTYSKSPAAQAGETTKAYQRPPIGTTAQ 180

Qy 181 PVTLQMLAVTVAVATPTTLPRPSPAASVTSIIPRQSVGHSQEMDLKSTATTYSS 237
Db 181 PVTLQMLAVTVAVATPTTLPRPSPAASVTSIIPRQSVGHSQEMDLKSTATTYSS 231

Qy 238 QNRPRADPGIQRQDPGSAAPQKPGVADVSLGLVPKBELSTQSLPEVSLGDPNCKIDLSPL 297
Db 232 -----PVLDD--SGFVPRBELSTQSSSEPVQGDNPCKIDLSPL 269

Qy 298 IDGSTSIGKRRFRIQKOLLADVAQALDIPAGPLMGVYQVQYGDNPATFNKLTHTNSRDLK 357
Db 270 IDGSTSIGKRRFRIQKOLLADVAQALDIPAGPLMGVYQVQYGDNPATFNKLTHTNSRDLK 329

Qy 358 TAIKTIQORGLSNVGRRAISFVTKNFFSKANGNRSGAPNVVVVMDGWPDKVBEASRLA 417
Db 330 TAIKTIQORGLSNVGRRAISFVTKNFFSKANGNRSGAPNVVVVMDGWPDKVBEASRLA 389
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QY 418 RESGINIPITIEGAARENEKQVVEPNFANKAVCRITNGFYSLHVQSWFGLHKTLOPLVKR 477
DB 390 RESGINVPIITVEGAARENEKQVVEPNFASKAVCRITNGFYSNVQSWLSLHKTIVQPLVKR 449
QY 478 VCDTRLACKTKCLNSADIGFVIDGSSSVGTGNFRITVLOFVFNLTKEFEISDTRIGAV 537
DB 450 VCDTRLACKTKCLNSADIGFVIDGSSSVGTGNFRITVLOFVFNLTKEFEISDTRIGAV 509
QY 538 QYTYEORLEFGFDKYSKPKDILNAIKRVGVWSGTSTGAAINPALEQKPKSKPKRKLKLM 597
DB 510 QYTYEORLEFGFDKYSKPKDILNAIKRVGVWSGTSTGAAINPALEQKPKSKPKRKLKLM 569
QY 598 ILIITDGRSYDDVRIPAMAAHKGVTIYAIQVAAQAQEELEVIATHPARDHSFFVDFFDL 657
DB 570 ILIITDGRSYDDVRIPAMAAHKGVTIYAIQVAAQAQEELEVIATHPARDHSFFVDFFDL 629
QY 658 HQVPRIIQNICTEFNSQPRN 678
DB 630 YKIAPRIIQNICTEFNSQPRN 650

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RESULT 5

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Q95LI2 ID Q95LI2 PRELIMINARY; PRT; 652 AA.
AC Q95LI2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vitrin.
OS Bos taurus (Bovine).
GN Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Ren Z.-X., Liu J.G., Mayne R.;
RT "Bovine vitrin cDNA sequence."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF063832; AAL18262.2; -.
DR InterPro; IPR004043; LCCL dom.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PSS0820; LCCL; 1.
DR PROSITE; PSS0234; VWA; 2.
SQ SEQUENCE 652 AA; 70872 MW; 3512421CA6987C51 CRC64;

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Query Match 80.5%; Score 2818; DB 6; Length 652;
Best Local Similarity 79.8%; Pred. No. 1.5e-193;
Matches 541; Conservative 49; Mismatches 62; Indels 26; Gaps 2;

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```

QY 1 MRTVLTMKASVTEMFLVLLVTGHSNKETAKKIKRPFVTPQINCVDKAGKIIDPEFIV 60
DB 1 MGIWVPTMKASVTEMFLVLLVTGHSNKETAKKIKRPFVTPQINCVDKAGKIIDPEFIV 60
QY 61 KCPAGCDPKYHVYGTVDYASVSCGAAVHSGVLDNSGGKILVRKVAGSGYKGSYNG 120
DB 61 KCPGCGDPRHYVYGVADYASVSCGAAVHSGVLDNSGGKILVRKVAGSGYKGSYNG 120
QY 121 VQSLSLPRWRRESFIVLSKPKKGVTPYPSALTYSSSKSPAQAAGTTKAYORPPIPGTTAQ 180
DB 121 VQSLSLPRWRRESFIVLSKPKKGVTPYPSALTYSSSKSPAQAAGTTKAYORPPIPGTTAQ 180
QY 181 PVTLMQLLATVAVATPTTLPRPSSAATSTISIPRQSVGHSRQEMDLSTATYTSSQNR 240
DB 181 PVTVTPAGTATBATHTTLTPKPSFASGTSAGSLRPPQAGQRSKDL----- 226

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QY 241 PRADPGIORQDPSGAARFQKPGVADVSLGVPKEELSTQSLPESVLSGDPNCKIDLSFLIDG 300
DB 227 --GEP-----ALWKPESVLLDAGFVPKEELSTQSLPESQDPSCKVDLSFLIDG 274
QY 301 STSISGRFRRIKOLLADVAQALDIGPAGPLMGVVOYGNPAPATHFNLTHTNSRDLKTAI 360
DB 275 SSSISGRFRRIKOLLADVAQALDIGPAGPLMGVVOYGNPAPATHFNLTHTNSRDLKTAI 334
QY 361 EKITORGGLSNVGRASISFVTNPFPSKANGRSGAPVVMVMDGWPDTDKVVERASRLARES 420
DB 335 EKISORGGLSNVGRASISFVTNPFPSKANGRSGAPVVMVMDGWPDTDKVVERASRLARES 394
QY 421 GINIPIITIEGAARENEKQVVEPNFANKAVCRITNGFYSLHVQSWFGLHKTLOPLVKRCD 480
DB 395 GVINIPIITIEGAARENEKQVVEPNFANKAVCRITNGFYSLHVQSWFGLHKTLOPLVKRCD 454
QY 481 TDLRACKTKCLNSADIGFVIDGSSSVGTGNFRITVLOFVFNLTKEFEISDTRIGAVOYT 540
DB 455 TDLRACKTKCLNSADIGFVIDGSSSVGTGNFRITVLOFVFNLTKEFEISDTRIGAVOYT 514
QY 541 YEOLEFGFDKYSKPKDILNAIKRVGVWSGTSTGAAINPALEQKPKSKPKRKLKMLI 600
DB 515 YEOLEFGFDKYSKPKDILNAIKRVGVWSGTSTGAAINPALEQKPKSKPKRKLKMLI 574
QY 601 TDGRSYDDVRIPAMAAHKGVTIYAIQVAAQAQEELEVIATHPARDHSFFVDFFDLHQY 660
DB 575 TDGRSYDDVRIPAMAAHKGVTIYAIQVAAQAQEELEVIATHPARDHSFFVDFFDLHQY 634
QY 661 VPRIIQNICTEFNSQPRN 678
DB 635 VPRIIQNICTEFNSQPRN 652

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RESULT 6

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Q8K047 ID Q8K047 PRELIMINARY; PRT; 650 AA.
AC Q8K047;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RIKEN cDNA 2810429K11 gene.
GN VIT OR 2810429K11RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034120; AAH34120.1; -.
DR MGD; MGI:1921449; Vit.
DR InterPro; IPR004043; LCCL dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PSS0820; LCCL; 1.
DR PROSITE; PSS0234; VWA; 2.
SQ SEQUENCE 650 AA; 70698 MW; 1641623B11003B48 CRC64;

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Query Match 80.0%; Score 2801; DB 11; Length 650;
Best Local Similarity 80.5%; Pred. No. 2.5e-192;
Matches 548; Conservative 40; Mismatches 59; Indels 34; Gaps 5;

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```

QY 1 MRTVLTMKASVTEMFLVLLVTGHSNKETAKKIKRPFVTPQINCVDKAGKIIDPEFIV 60
DB 1 MGIWVPTMKASVTEMFLVLLVTGHSNKETAKKIKRPFVTPQINCVDKAGKIIDPEFIV 60

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QY 61 KCPACQDPKHYVCTDVVYSSVCGAAVHSGVLDNSGGKILVRKVGQSGYKGSYNG 120
Db 61 KCPACQDPKHYVCTDVVYSSVCGAAVHSGVLDNSGGKILVRKVGQSGYKGSYNG 120
QY 121 VQSLSLPWRESFVILESKPKGVVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
Db 121 VQSLSLPWRESFVILESKPKGVVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
QY 181 PVTLMQLAVTVATPPTLPSPSAATSTSIIPRQSVGHSQEM---DLWSTATYTS 237
Db 181 PVTLMQLAVTVATPPTLPSPSAATSTSIIPRQSVGHSQEM---DLWSTATYTS 237
QY 238 QNRPRADPGIQRDPSGAAPQKPVGADVSLGLVPEELSTQSLVPSLGDGPNCKIDLSFL 269
Db 238 QNRPRADPGIQRDPSGAAPQKPVGADVSLGLVPEELSTQSLVPSLGDGPNCKIDLSFL 269
QY 298 IDGSTSIGRRFRIQKQLLADVAQALDIPAGPLMGVVOYGNPAPATHFNLTHTNSRDLK 357
Db 298 IDGSTSIGRRFRIQKQLLADVAQALDIPAGPLMGVVOYGNPAPATHFNLTHTNSRDLK 357
QY 270 IDGSTSIGRRFRIQKQLLADVAQALDIPAGPLMGVVOYGNPAPATHFNLTHTNSRDLK 329
Db 270 IDGSTSIGRRFRIQKQLLADVAQALDIPAGPLMGVVOYGNPAPATHFNLTHTNSRDLK 329
QY 358 TAIEKITQGGLSNVGRAISFVTKNFFSKANGNRGAPNVVVMVDGWPDKVBEASRLA 417
Db 358 TAIEKITQGGLSNVGRAISFVTKNFFSKANGNRGAPNVVVMVDGWPDKVBEASRLA 417
QY 330 TAIEKITQGGLSNVGRAISFVTKNFFSKANGNRGAPNVVVMVDGWPDKVBEASRLA 389
Db 330 TAIEKITQGGLSNVGRAISFVTKNFFSKANGNRGAPNVVVMVDGWPDKVBEASRLA 389
QY 418 RESGINIFITIEGAAREKQVVPNPANKAVCRNTNGFYSLVHVSFGLHKTLOPLVCR 477
Db 418 RESGINIFITIEGAAREKQVVPNPANKAVCRNTNGFYSLVHVSFGLHKTLOPLVCR 477
QY 390 RESGINVFFITVEGAAREKQVVPNPANKAVCRNTNGFYSLVHVSFGLHKTLOPLVCR 449
Db 390 RESGINVFFITVEGAAREKQVVPNPANKAVCRNTNGFYSLVHVSFGLHKTLOPLVCR 449
QY 478 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKFEFISDTDTIGAV 537
Db 478 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKFEFISDTDTIGAV 537
QY 450 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKFEFISDTDTIGAV 509
Db 450 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKFEFISDTDTIGAV 509
QY 538 QYTYEQRLEFGDPKYSKPDILNAIKRVYVSGGTSFGAAINPALSQPKSPKPKRKL 597
Db 538 QYTYEQRLEFGDPKYSKPDILNAIKRVYVSGGTSFGAAINPALSQPKSPKPKRKL 597
QY 510 QYTYEQRLEFGDPKYSKPDILNAIKRVYVSGGTSFGAAINPALSQPKSPKPKRKL 569
Db 510 QYTYEQRLEFGDPKYSKPDILNAIKRVYVSGGTSFGAAINPALSQPKSPKPKRKL 569
QY 598 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARHSPVDFDFNL 657
Db 598 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARHSPVDFDFNL 657
QY 570 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARHSPVDFDFNL 629
Db 570 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARHSPVDFDFNL 629
QY 658 HOYVPRIIQNICTEFNSOPRN 678
Db 658 HOYVPRIIQNICTEFNSOPRN 678
QY 630 YKIAPRIIQNICTEFNSOPRN 650
Db 630 YKIAPRIIQNICTEFNSOPRN 650

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RESULT 7

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Q9CYZ1
ID Q9CYZ1 PRELIMINARY; PRT; 650 AA.
AC Q9CYZ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 2810429Klik protein.
GN VIT OR 2810429KLIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saico T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saico R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA Guetincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
RA Hayashizaki Y.,
RT *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
DR EMBL; AK013193; BAB28702.1; -.
DR HSSP; P17301; LAOX.
DR MGD; MGI:1921449; Vit.
DR InterPro; IPR004043; LCCL_dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PRO0453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50334; VWF; 2.
SQ SEQUENCE 650 AA; 70638 MW; 03B4823E111A214B CRC64;
Query Match 79.8%; Score 2796; DB 11; Length 650;
Best Local Similarity 80.5%; Pred. No. 5, 7e-192;
Matches 548; Conservative 39; Mismatches 60; Indels 34; Gaps 5;
QY 1 MRTVVLTKASVIEMLVLLVTGVHSHNKETAKKIKRPKFTVPQINCVDVXAGKIIDPEFIV 60
Db 1 MGIIVVPTMKASVIEVLLVLLVTGHSNKETPKTKRPLKTVQINCVDVXAGKIINPEFV 60
QY 61 KCPACQDPKHYVCTDVVYSSVCGAAVHSGVLDNSGGKILVRKVGQSGYKGSYNG 120
Db 61 KCPACQDPKHYVCTDVVYSSVCGAAVHSGVLDNSGGKILVRKVGQSGYKGSYNG 120
QY 121 VQSLSLPWRESFVILESKPKGVVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
Db 121 VQSLSLPWRESFVILESKPKGVVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
QY 181 PVTLMQLAVTVATPPTLPSPSAATSTSIIPRQSVGHSQEM---DLWSTATYTS 237
Db 181 PVTLMQLAVTVATPPTLPSPSAATSTSIIPRQSVGHSQEM---DLWSTATYTS 237
QY 238 QNRPRADPGIQRDPSGAAPQKPVGADVSLGLVPEELSTQSLVPSLGDGPNCKIDLSFL 297
Db 238 QNRPRADPGIQRDPSGAAPQKPVGADVSLGLVPEELSTQSLVPSLGDGPNCKIDLSFL 297
QY 232 -----PG-----FVLLD---SGFVPKPEELSTQSSBPVQGDPNCKIDLSFL 269
Db 232 -----PG-----FVLLD---SGFVPKPEELSTQSSBPVQGDPNCKIDLSFL 269
QY 298 IDGSTSIGRRFRIQKQLLADVAQALDIPAGPLMGVVOYGNPAPATHFNLTHTNSRDLK 357
Db 298 IDGSTSIGRRFRIQKQLLADVAQALDIPAGPLMGVVOYGNPAPATHFNLTHTNSRDLK 357
QY 270 IDGSTSIGRRFRIQKQLLADVAQALDIPAGPLMGVVOYGNPAPATHFNLTHTNSRDLK 329
Db 270 IDGSTSIGRRFRIQKQLLADVAQALDIPAGPLMGVVOYGNPAPATHFNLTHTNSRDLK 329
QY 358 TAIEKITQGGLSNVGRAISFVTKNFFSKANGNRGAPNVVVMVDGWPDKVBEASRLA 417
Db 358 TAIEKITQGGLSNVGRAISFVTKNFFSKANGNRGAPNVVVMVDGWPDKVBEASRLA 417
QY 330 TAIEKITQGGLSNVGRAISFVTKNFFSKANGNRGAPNVVVMVDGWPDKVBEASRLA 389
Db 330 TAIEKITQGGLSNVGRAISFVTKNFFSKANGNRGAPNVVVMVDGWPDKVBEASRLA 389
QY 418 RESGINIFITIEGAAREKQVVPNPANKAVCRNTNGFYSLVHVSFGLHKTLOPLVCR 477
Db 418 RESGINIFITIEGAAREKQVVPNPANKAVCRNTNGFYSLVHVSFGLHKTLOPLVCR 477
QY 390 RESGINVFFITVEGAAREKQVVPNPANKAVCRNTNGFYSLVHVSFGLHKTLOPLVCR 449
Db 390 RESGINVFFITVEGAAREKQVVPNPANKAVCRNTNGFYSLVHVSFGLHKTLOPLVCR 449
QY 478 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKFEFISDTDTIGAV 537
Db 478 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKFEFISDTDTIGAV 537
QY 450 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKFEFISDTDTIGAV 509
Db 450 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVNTLTKFEFISDTDTIGAV 509
QY 538 QYTYEQRLEFGDPKYSKPDILNAIKRVYVSGGTSFGAAINPALSQPKSPKPKRKL 597
Db 538 QYTYEQRLEFGDPKYSKPDILNAIKRVYVSGGTSFGAAINPALSQPKSPKPKRKL 597
QY 510 QYTYEQRLEFGDPKYSKPDILNAIKRVYVSGGTSFGAAINPALSQPKSPKPKRKL 569
Db 510 QYTYEQRLEFGDPKYSKPDILNAIKRVYVSGGTSFGAAINPALSQPKSPKPKRKL 569
QY 598 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARHSPVDFDFNL 657
Db 598 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARHSPVDFDFNL 657
QY 570 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARHSPVDFDFNL 629
Db 570 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARHSPVDFDFNL 629
QY 658 HOYVPRIIQNICTEFNSOPRN 678
Db 658 HOYVPRIIQNICTEFNSOPRN 678
QY 630 YKIAPRIIQNICTEFNSOPRN 650
Db 630 YKIAPRIIQNICTEFNSOPRN 650

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```
Db 630 YKIAPRIIIONICTEFNSQPRN 650
RESULT 8
Q8BQ41
ID Q8BQ41 PRELIMINARY; PRT; 628 AA.
AC Q8BQ41;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE VITRIN.
GN VIT OR 2810429KJ11RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;
RC MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK051606; BAC34688.1; -.
DR MGD; MGI:1921449; Vit.
DR InterPro; IPR004043; LCCL.dom.
DR InterPro; IPR002035; VWP_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWPADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWA; 2.
DR PROSITE; PS50234; VWA; 2.
SQ SEQUENCE 628 AA; 68198 MW; C96C4ACB9E72480 CRC64;

Query Match 76.6%; Score 2682; DB 11; Length 628;
Best Local Similarity 77.7%; Pred. No. 8.2e-184;
Matches 529; Conservative 39; Mismatches 57; Indels 56; Gaps 6;

Qy 1 MRTVLTAKASVIEKFLVLLVTGSHNKEAKKIIRPKFTVPQINCVDKAGKIIDPEFIV 60
Db 1 MGIVVPTMKASVIEVLL-----AVPQINCVDKAGKIINPEFV 38

61 KCPAGCQDPKHYVTDVYASVYSCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG 120
39 KCPAGCQDPKHYVGTGYASVYSCGAAIHSGVLDNSGGKILVRKVAGQSGYKGSYNG 98

121 VQSLSPWRRESFVLESKPKKGVTPSALTYSSKSPAAQAGETTKAYORPPINGITPAQ 180
99 VQSLSPWRRESFVLESKPKKGVTPSALTYSSKSPAAQAGETTKAYORPPINGITPAQ 158

181 PVTLMQLAVTVAVATPTTLPRPSPASASTTSIPRQSVGHRSQEM---DLWSTATYSS 237
159 PVTLMQLAVTVAVATPTTLPRPSPASASTTSIPRQSVGHRSQEM---DLWSTATYSS 209

238 QNRPRADPGIORQDPGSGAFAQKPGVADVSLGLVPKEELSTOSLBPVSLGDPNCKIDLSP 297
210 -----PG-----PVLID--SGFVPKEELSTOSLBPVSGDQPNCKIDLSP 247

298 IDGSTSICKRPRFRIQKQLADVAQALDIPAGPLGVVQYQGNPATFNKTHNSRDLE 357
248 IDGSTSICKRPRFRIQKQLADVAQALDIPAGPLGVVQYQGNPATFNKTHNSRDLE 307

358 TAIEKIQRGGLSNVGRASIFVTKNPFPSKANGNRSAGPVMVVDGWPPTDKVEASRLA 417
308 TAIEKIQRGGLSNVGRASIFVTKNPFPSKANGNRSAGPVMVVDGWPPTDKVEASRLA 367

418 RESGINPFITTEGAENEKQYVVEPNFANTAVCTNGFSYLIHQSWFGLHKTLOPLVKR 477
368 RESGINPFITTEGAENEKQYVVEPNFANTAVCTNGFSYLIHQSWFGLHKTLOPLVKR 427
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```
Qy 478 VCDTDLRACSKTCLNSADIGFVIDGSSSVGNGFRFTVLQFVTNLTKFEIISDTTRIGAV 537
Db 428 VCDTDLRACSKTCLNSADIGFVIDGSSSMGTSNFRFTVLQFVANLSKEFEISDTTRIGAV 487
Qy 538 QYTYEORLEFGPKYSSKPDILNAIKVGVYWSGGTSTGAAINFALBQLPKSKPKNRKLM 597
Db 488 QYTYEORLEFGPKYSSKPDILNAIKVGVYWSGGTSTGAAINFALBQLPKSKPKNRKLM 547
Qy 598 ILITDGRSYDDVRIPAMAHLKGVITYAIGVAMAQBELEVIATHPARDHSFFVDFDNL 657
Db 548 ILITDGRSYDDVRIPAMAHLKGVITYAIGVAMAQBELEVIATHPARDHSFFVDFDNL 607
Qy 658 HQYVPRIIIONICTEFNSQPRN 678
Db 608 YKIAPRIIIONICTEFNSQPRN 628

RESULT 9
Q8AW56
ID Q8AW56 PRELIMINARY; PRT; 553 AA.
AC Q8AW56;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SI:d2234G15.4 (Novel protein similar to coagulation factor C homolog
DE (Cochlin, COCH)).
GN SI:d2234G15.4.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Babbage A.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL596026; CAD58748.1; -.
DR InterPro; IPR004043; LCCL.dom.
DR InterPro; IPR002035; VWP_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWPADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWA; 2.
DR PROSITE; PS50234; VWA; 2.
SQ SEQUENCE 553 AA; 60351 MW; 4A3B136747C488P0 CRC64;

Query Match 33.9%; Score 1187.5; DB 13; Length 553;
Best Local Similarity 37.7%; Pred. No. 1.3e-76;
Matches 251; Conservative 107; Mismatches 184; Indels 123; Gaps 8;

Qy 16 FLVLIVLVGVHS-----NKETAKKIKRPFVTPQINCVDKAGKIIDPEFIVKCPAGCQDPKY 71
Db 5 FAVILVILGLISLWCTSGSELNVA TP-----ISGTRAVLSDTHLILVCPANCLASL 58

72 HVGTDVYASVYSCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSPWR 131
59 SVFGSGVYASISSICGAHHRGIIIGLSGPPVEVHGLQGRITVLSYAHGVQSLSQNSA 118

132 SFVLESKPKKGVTPSALTYSSKSPAAQAGETTKAYORPPITGTAQPTLMQLAVT 191
119 SF----- 120

192 VAVATPTTLPRPSPASASTTSIPRQSVGHRSQEMDLWSTATYSSQNRPRADPGIOR 251
121 -TVARTISLPLEVSSQTSSSAIV----- 142

252 PSGAFAQKPGVADVSLGLVPKEELSTOSLBPVSLGDPNCKIDLSPILDGSTSI 311
143 ASGAA-KFVPVK-----IVKK-----PPPATAHKDCPVDMLLDSSVYNGQRFPNL 188
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QY 312 QKOLLADVAQALDIPAGPAGLVGVQYQNDPNATHFNKLTHTNSRDLKTAIEKITORGGLSN 371
DB 189 QKNFVSKLMLKVGTOGPHVGVQTSPTPTFTYLTNTAKDVTFAIKEIPIYGCNTN 248
QY 372 VGRAISFVTKNPFSSKANGRSAGNPNVVMVDCWPTDKVEASRLARESGINIPFITIEG 431
DB 249 TGKAILHTVRPFPDFGVRGYPYVIVFDWPNFSDNVEEAAIILARESGINIPFVSVAK 308
QY 432 AARENEKQYVWPNFANKAVCRTNGYSYLVHVSFVGLHKTLOPLVKRVCDDTORLACSKTCL 491
DB 309 PSPEASLVSDQDFMRKAVCKDNEFTTMSWFSNFKVPLKLSIDQMLCKTICY 368
QY 492 NSADIGFVIDSSSVGTGNFTVLQFVNTLTKFEISDTRIGAVQYTYEORLEFGDK 551
DB 369 NSVDLGLFIDSSVGDGNFRLVLLVLSIARSFDISDGRIGAIQTYDQRMFEFNND 428
QY 552 YSSKPDILNAIKRVYMSGSGTSTGAINFALFOLFKKFKPKRKLMLITDGRSYDDVRI 611
DB 429 HVLKDNALRALQKIPYMSGGTATGDAINFARSLPKPRSSNRKPLIITDQSYDDVRI 488
QY 612 PMAAHLKGVITYAIGVAAQAELEVLATHPARHSFFVDFDNLHGVVPRIIQNIC-- 669
DB 489 PMAAQRGIGITYAVGVAAWAPMEDLKAMASEPKESHVFTTFTGLGQFQOPVIRGICRD 548
QY 670 -TEFN 673
DB 549 FTEFN 553

RESULT 10
Q961U6 PRELIMINARY; PRT; 494 AA.
AC Q961U6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Coagulation factor C (Limulus polyphemus) homolog (Cochlin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007230.1; -.
DR InterPro; IPR004043; LCCL_dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS08020; LCCL; 1.
DR PROSITE; PS0234; VWFA; 2.
SQ SEQUENCE 494 AA; 53230 MW; 9920BEF97A0AF2FF CRC64;

Query Match 29.1%; Score 1017.5; DB 4; Length 494;
Best Local Similarity 37.2%; Pred. No. 1.7e-64;
Matches 214; Conservative 90; Mismatches 153; Indels 119; Gaps 7;

QY 44 INCVDKAGKIIDPEPIVKPCAGQDPKHYVTVGVYASVSSVCGAAVHSGVLDNSGGKIL 103
DB 32 ITCFTRGIDIRKKEADVLCPGECPLREBSVGNIVYASVSSICGAARHGVINSGGPVR 91
QY 104 VRKVGQSGYKSGVNGVQSLSPWRBSFVILESKPKKGVITYPSALYSSKSPAAQAG 163
DB 92 VYSLPGRENYSDVDANGIOSQMLSEWSASFVTKCK-----SSTQATQA- 137
QY 164 ETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVATPTLPRPSPSAATSTIPRPQSVGHR 223
DB 138 -----VSTAHF----- 143

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RESULT 11

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Q7SYT5 PRELIMINARY; PRT; 490 AA.
ID Q7SYT5;
AC Q7SYT5;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshikiyuki S., Cantinci P., Prange C.,
RA Raba S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Maman A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;

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us-10-063-688-34.rspt

Search completed: May 27, 2004, 16:47:03
Job time : 54 secs

Search completed: May 27, 2004, 16:47:03
Job time : 54 secs


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; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-227

Query Match 32.3%; Score 1129.5; DB 4; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.8e-97;
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

Qy 44 INCVDKAGKIIDPEFIVKCPAGCQDPKHYHYGTDVYASVSCGAAVHSGVLDNSGKIL 103
Db 32 ITCTFRGLDIRKEKADVLCPGCGPLEBFSYGVNIVYASVSSICGAAVHRGVINSGGPVR 91
Qy 104 VRKVGQSGYKSGVNSGVQSLSPRRRESFVLESKPKGVTPYSALTYSSSKSPAAQAG 163
Db 92 VYSLPGRNYSYVDANGIOSQLSRMSASFVTKGK-----SSTQBATQA- 137
Qy 164 ETTKAYQRPPIGTTAQPVTLMQLLAVTAVATPTTLPRPSPSAATSTTIPRQSVGHR 223
Db 138 -----VSTAH- 143
Qy 224 QEMDLWSTATYTSQNRPRADPGIQRODPGAAFPQKPVGDVADVSIGLVPKEELSTQSL 283
Db 144 -----PTGKRLKK-----TPEKK----- 156
Qy 284 SLGDPNCKIDSLFIDGSTIGKRRFRIQKOLLADVAQALDIDGAPGLMGVQYGNPAT 343
Db 157 -TGKDCCKADIAFLIDGSFNIQGRFNLQNFVKGKVALMLGIGTEGPHVGLVQASEHPKI 215
Qy 344 HFNLKTHTNSDLKTAIEKLTORGSLNVRGAISFVTKNPSKXANGNRSGAPNVVVVMD 403
Db 216 EFLKNTSAKDLFALKEVGFGRGNSNTGKALKHTAQTFFVDAGVRKGIPKVVVVFFID 275
Qy 404 GWPTDKVEEASRLARESGINIFPTTIRGAENEKQYVYVEFNFAKVCRTNGFVSLHVQS 463
Db 276 GWFSDDIERAGIVAREEGVNVFVSVAKPIPEELGMQVDVTFDKAVCRNNGFSEYMPN 335
Qy 464 WFLHKTQLPVRKVCOTDLRACSKTCLNSADIGFVIDGSSSVGTGFRFVLOFVTLTK 523
Db 336 WFGTTKVKVPLVQKCLTHEQWMSKTCVNSVNTAFLIDGSSSVGDSNFRMLRLEFVSNIAK 395
Qy 524 EFEISDTRTRIGAVQYTYEQLRFGFKYSSKPDILNAIKRVGVNSGTTGAINFALE 583
Db 396 TFEISDIGAKIAAQQYTDQRTESFTDYSTKENVLAVIRNIRYMSGGTATGDAISFTVR 455
Qy 584 QLPR--KSKPKRKLMLITDGRSYDVRIPAMAHLKGVITTAIGVAAQAQEELEVIAT 641
Db 456 NVFGPIRESNPK-NFLVITVDGQSYDDVQGPAAAHADAGITIFSVGVAAFLDLDKMAS 514
Qy 642 HPARDHSFFVDFEONLHQYVPRITQICTEF 672
Db 515 KPKEASHAFFTEFTGLEPIVSDVIRGICRDP 545

RESULT 3
US-09-902-775A-227
; Sequence 227, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

```

Qy	224	QEMDLWSTATYTSSQNRPRADPGIORQDPGSAQKPKGVADSVLGLVPKEELSTQSLEPV	283
Db	144	----- : : -----TPKK-----156	
Qy	284	SLGDPNCKIDLFLIDGSTSIGKREFRIOKQLLADVAQALDIGPAGPLMGVVOYQDNPAT	343
Db	157	----- : : -----TPKK-----156	
Qy	344	HFNLKTHTSRDLKTAIEKITORGGLSNVGRAISFVTKPFKSKANGNRSGAPVWVVOVD	403
Db	216	EFYLNKFTSAKOVLPFAIKVEVGRGNSNTGKALKHTAQKFTVDAGYKRGPKVWVVPID	275
Qy	404	GWPTDKVEEASRLARESGINIFETIEGAAENKQYVVEPNFANKAVCRNTPGFVSLHVOS	463
Db	276	GWPSDDIEBAGIVAREPGVNVFVSVAPKPIBELGWQDVTFDKAVCRNNGFFSYHKN	335
Qy	464	WFLGHLTKLOPLVKRCDTDLRLACSKTCLNSADIGFVIDGSSSVGTGNPRIVLOFVTNLTK	523
Db	336	WFGTTRYKVPLOKLCTHEOMMCKNTCYNVNIAFLIDGSSSVGDSNFRMLMFLPVSNIK	395
Qy	524	EPHISTDTRIGAVQYTYEORLEFGFDKYSKKPDILINAIKEVGYWSGGTSTGAJNPAL	583
Db	396	TPEISDIGAKIAAOPVTDQRTFESFTDYSTKENVLAVIRNIRYMSGGTATGDAISFTVR	455
Qy	584	QLAF--KSPNKGKMLMILTDCRSYDDVRIIPAMAHLKGVITYAIGVAMAAQEELEVAT	641
Db	456	NFGPPIRESFNK-NFLVIVTDOQSDDVQGPAAAAHADGIIYTFSGVAMAFPLDLKMAS	514
Qy	642	HPARDHSFFVDFDNLHVOYPIIIONICTEP	672
Db	515	KPKESHAPFTREFTGLEPVSVDVIRGICRDP	545

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RESULT 4
US-08-462-128-37
: Sequence 37, Application US/08462128
: Patent No. 5686059
: GENERAL INFORMATION:
: APPLICANT: Goetinck, Paul F.
: APPLICANT: Tondravi, Mehrdad
: TITLE OF INVENTION: CARTILAGE MATRIX PROTEIN AND METHODS FOR
: TITLE OF INVENTION: USE
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lahive & Cockfield
: STREET: 60 State Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER: US/08/462,128
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/006,096
: FILING DATE: 15-JAN-1993
: APPLICATION NUMBER: US 07/866,403
: FILING DATE: 10-APR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Myers, Paul L.
: REGISTRATION NUMBER: 35,965
: REFERENCE/DOCKET NUMBER: MGP-005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 37:
: SEQUENCE CHARACTERISTICS:

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; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,443
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0348 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1732121
; US-08-897-443-4

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Query Match      14.3%  Score 501.5;  DB 2;  Length 496;
Best Local Similarity 28.8%; Pred. No. 2.8e-38;
Matches 129; Conservative 80; Mismatches 178; Indels 61; Gaps 9;

QY 273 HELSTQSLFVSLGDPNCK---IDLSPIDGSTIGKRRFRIOKQLADVAQALDIPGAG 329
DB 19 QALCSPCLAPQSRGH-LCTRPTDLVFPVDSRSVRPVEFEKVKVPFSLQVIESLDVGPN 77

QY 330 PLMGVVOYGNPNATHNLKTHNSRDLKTAIEKITQGGLSNVGRRAISFVTKNPFPSKANG 389
DB 78 TRVGMVNYASTVRQEFSLRAHVSKAALLQAVRIQPLSTGTMTGLAIQFAITKAFDABG 137

QY 390 NRSGAPN---VVVMVDGMPDKVERASRLARESGINIPTITIGAAENE--KQVYVPEPN 444
DB 138 GRSRSPDISKVIWVTDGRPDQSVQDVASARASGVFELPAIGV-GSVDKATLRQIASEPQ 196

QY 445 FANKAVCRITNGFYSLHVSQWFGHLKTLQP-----LVKRVCDTDRLACSKTCLNS----- 493
DB 197 DEHVD-----YVESYSVIEKLSRKFEQAPCVVSDLCATGDHDCBQVCISSPGSYT 246

QY 494 -----ADTGFVIDGSSSVGTGNFRTVLPVFNLTKEFE 526
DB 247 CACHGFTLNSDGKTCNVCSSGGSSATDLVFLIDGSKSVRPENFELVKKFIQIVDTLD 306

QY 527 ISDTDFRIGAVOYTYEORLEFGDKYSSKPDILNAIKRVGWSGGTGTGAALNFBALBOLF 586
DB 307 VSDKLAQGLVQYSSSVRQEPFLGRFHTKDDIKAAVRNMSYMEKGTWTGAALKYLDNSP 366

QY 587 KKS---KPNKRKLMILITDGRSDYDDVRIPAPMAAHLKGVITYAIGVAAQAQBELEVIATHP 643
DB 367 TVSSGARPQAQKVGIVFTDGRSQDYINDAAKAKDLGFKMFVGVGVNAVEDELREIASBP 426

QY 644 ARHSPFVDFDNLHQVRIQNICTE 671
DB 427 VAEHYFTADFKTINQIGKKLQKICVE 454

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RESULT 8
US-08-463-218-1

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; Sequence 1, Application US/08463218
; Patent No. 5986052
; GENERAL INFORMATION:
; APPLICANT: Goetinck, Paul F.
; APPLICANT: Tondravi, Mehrdad
; APPLICANT: Binette, Francois
; TITLE OF INVENTION: METHODS FOR PROMOTING CARTILAGE MATRIX
; TITLE OF INVENTION: FORMATION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,218
; FILING DATE: 05-JUNE-1995
; PRIOR APPLICATION DATA: US 08/001,078
; APPLICATION NUMBER:
; FILING DATE: 06-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-008DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-463-218-1

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Query Match      14.3%  Score 501.5;  DB 2;  Length 496;
Best Local Similarity 28.8%; Pred. No. 2.8e-38;
Matches 129; Conservative 80; Mismatches 178; Indels 61; Gaps 9;

QY 273 HELSTQSLFVSLGDPNCK---IDLSPIDGSTIGKRRFRIOKQLADVAQALDIPGAG 329
DB 19 QALCSPCLAPQSRGH-LCTRPTDLVFPVDSRSVRPVEFEKVKVPFSLQVIESLDVGPN 77

QY 330 PLMGVVOYGNPNATHNLKTHNSRDLKTAIEKITQGGLSNVGRRAISFVTKNPFPSKANG 389
DB 78 TRVGMVNYASTVRQEFSLRAHVSKAALLQAVRIQPLSTGTMTGLAIQFAITKAFDABG 137

QY 390 NRSGAPN---VVVMVDGMPDKVERASRLARESGINIPTITIGAAENE--KQVYVPEPN 444
DB 138 GRSRSPDISKVIWVTDGRPDQSVQDVASARASGVFELPAIGV-GSVDKATLRQIASEPQ 196

QY 445 FANKAVCRITNGFYSLHVSQWFGHLKTLQP-----LVKRVCDTDRLACSKTCLNS----- 493
DB 197 DEHVD-----YVESYSVIEKLSRKFEQAPCVVSDLCATGDHDCBQVCISSPGSYT 246

QY 494 -----ADTGFVIDGSSSVGTGNFRTVLPVFNLTKEFE 526
DB 247 CACHGFTLNSDGKTCNVCSSGGSSATDLVFLIDGSKSVRPENFELVKKFIQIVDTLD 306

QY 527 ISDTDFRIGAVOYTYEORLEFGDKYSSKPDILNAIKRVGWSGGTGTGAALNFBALBOLF 586
DB 307 VSDKLAQGLVQYSSSVRQEPFLGRFHTKDDIKAAVRNMSYMEKGTWTGAALKYLDNSP 366

QY 587 KKS---KPNKRKLMILITDGRSDYDDVRIPAPMAAHLKGVITYAIGVAAQAQBELEVIATHP 643
DB 367 TVSSGARPQAQKVGIVFTDGRSQDYINDAAKAKDLGFKMFVGVGVNAVEDELREIASBP 426

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Query Match	10.6%	Score 370;	DB 4;	Length 915;
Best local Similarity	17.9%;	Pred. No. 1.9e-25;		
Matches 139;	Conservative 81;	Mismatches 191;	Indels 364;	Gaps 133
Qy	256	AFQKPVGADVSLGLVPKEELSTQSLSPVSLGDPNCKIDLSFLIDGSTSIGKRRPRIOKOL	315	
Db	23	ARERSGRSISGRHARTHPTALLES---SCENKRALDVLIIIDSSRVNTHYAKVKEP	79	
Qy	316	LADVAQALDIDGAPGLMGVVOYGDNPATFNKLKTHTNSRDLKTALEKIQTQSGLSNVGRA	375	
Db	80	IVDILQFLDIDGPDVTRVGLLQVSGTVKNFSLKTPRKSEVERAVERMHLSTGTMTGLA	139	
Qy	376	ISPVTKAPFSSXANGN---RSGAPVVVVVMDGWPTDKVEEASRLARESGINIF	425	
Db	140	IQYALNTAFSAEGARPLRENVPRVIMITVDGRPODSVAEVAAKARDTGILLFALGVGV	199	
Qy	426	-FTIE--GAENEEKQVVEPNF	445	
Db	200	DFNTILKSIGSEPHEDHVPZLVANFSQIETLTSVPQKCLTAHMCSTLEHCAHFCLINIPGS	259	
Qy	446	-----ANKAVCR	452	
Db	260	YVCRCKQGYILNSDQTCRIQDLCAMEDHNCQLCVNVPGSFVQCYSYALAEADGKCV	319	
Qy	453	-----TNGFSLFVGSWGL	467	
Db	320	AVDYCASENHGCEHCVCNADGSLYCQCHGFPALNPDKTCRINYCALNKPGCGEHCVCNM	379	
Qy	468	-----HK--TLQP	475	
Db	380	EESYVCRCHGYTLLDPNGKTCRVVDHCAQDHGCEQLCLNTEDSPVQCSEBGLINEDLK	439	
Qy	476	-----	475	
Db	440	TCSRVDYCLLSDHGCEYSCVNMDRSPACQCPGHHVLRSDGKTCAKLSDSCALGDHGHCHSC	499	
Qy	476	-----	475	
Db	500	VSSBDSFVQCQPEGYILBEDGKTCRRKDVQCAIDHGCEHI CVNSDDSTCECLEGFRLAIE	559	
Qy	476	-----KRVCDTDLRACSKTCLNSA	500	
Db	560	DGKRCRRKDVKCSITHHGCEHI CVNNGNSYICKSBSGFVLAEGRCKKCTEGPIDLAVFWI	619	
Qy	501	DGSSSVGTGNFVTLQFVTNLTKPEIISDTDRIGAVQVYTBQRLBFGDKYSSFPDILN	560	
Db	620	DGSKSLGSENFVWQVFTGIIDSLTISPKAARVGLLQVSTQVHTFTLRNFSNARDMKK	679	
Qy	561	AIKRVGVSGGTSTCAANPALEQLFKK---SKPNKRKL---MILITDGRSVDVDRIPAM	614	
Db	680	AVAHMCKMGKSMTGLALKHMFERSFTQEGGARPLSTRVPRAAI VFTDGRAQDDVSEWAS	739	
Qy	615	AAHLKGVTIYAIGWAAQAEELLEVIAITHAPDHSFFVDFSDNLQHVQVPRIIQNIC	669	
Db	740	KAKANGITWYAVGVCKAIABEELOBIASEPNTKHLFVAFDFSTWDBISEKLGKGC	794	

RESULT 11
US-09-905-125A-34
; Sequence 34, Application US/09905135A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

```

: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/905,125A
: CURRENT FILING DATE: 2001-07-12
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 34
: LENGTH: 915
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-905-125A-34

Query Match      10.64; Score 370; DB 4; Length 915;
Best Local Similarity 17.9%; Pred. No. 1.9e-25;
Matches 139; Conservative 81; Mismatches 191; Indels 364; Gaps 13

QY      256  AFQKPVGADYSLGLVPKKEELSTQSLPVSGLDPNCKDLSFLIDGSTSIGKRRPRIQKQL 315
DB      23  ARESRGRSISGRGHARTHPQTALLS---SCENKRADLVFIILSSRSVNTHDYAKVKEP 79
QY      316  LADVAQALDIDGAPGLMGVQYQGNPATHFNLTKHTNTSRDLKTAIEKITORGGLSNVGRA 375
DB      80  IVDILQFLDIDGPVTRVGLLQYGVSTVKNFEKSLTKFKKSEVERAVKMRHLSTGTMTGLA 139
QY      376  ISFVTKNFFSKANGN---RSGAPNVVVMMVQGWPTDKVEBASRLARESGINIF----- 425

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Db 140 IYALNIAFSEAEAGARPURENVRVIMIVTDGRPODSVAEAAKARDTGILIFAIQGVGV 199
Qy -FITIE--GAENKQYVVEPNF----- 445
Db 200 DFNTLKSIGSEPHEDHVLVAFNSQIETLTSVFQKCLTAHMCSTLEHCAHFCINIPGS 259
Qy 446 -----ANKAVCR----- 452
Db 260 YVCRCKQGYILNSDQTTCTRIQDLCAEDHNCBQLCVNVPSPVCCYGYALAEDEKRCV 319
Qy 453 -----TNGFYSLHVQSWFGL----- 467
Db 320 ADVYCASNHGCEHCVCNADGSLYCQCHGFAINPDEKTCRINVCALNKPGEHCVCNM 379
Qy 468 -----HK--TLQP----- 475
Db 380 EESYVCRCHRGVTLDPNGKTCRVHDCAQDHGCEQLCINTEDSFVCCSEGFILNEDLK 439
Qy 476 ----- 475
Db 440 TCSRVDYCLLSDHGCEYSCVNDRSFACQCPGHEVLRSDGKTCAMLDSCALGDHGEHSC 499
Qy 476 ----- 475
Db 500 VSEDSFVCCPFGVYLRDGGKTCRKDVQCAIDHGCHEHCVNSDSYTCSEGLEFRLA 559
Qy 476 -----KRVCDTRLACKSKCLNSA-----DIGFVI 500
Db 560 DGKCRKRDVCKSTHGHCEHCVCNNGNSYICKSEGFVLAEDGRCKCTGPGIDLVPVI 619
Qy 501 DGSSSVGNGRFRVTLQVFNLTKEFEISDVTDRIGAVQYTYEORLEFGDFKYSSKPDILN 560
Db 620 DGSKSLGENFEWVKQFVTGIIDSITSPKAAVGLLQVSTQVHTPTLRNFNSAKOMKK 679
Qy 561 AKRVGWSGTSTGAALNPALEQLFKK---SKWKRKL---MILITGRSYDDVRIIPAM 614
Db 680 AVAHMYKMGKSMTGALAKHGFERSPTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWAS 739
Qy 615 AAHLKGVTVYIAGVMAAOEELVATHPARDHSFVDFEFTNLHQYVPRITONIC 669
Db 740 KAKANGITWYAVGVGAKEERLQELIASEPTWKHLFYAEDFTMDIEISKLKKGIC 794

RESULT 12

US-09-902-775A-34
; Sequence 34, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Pao, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

Query Match 10.6%; Score 370; DB 4; Length 915;
Best Local Similarity 17.9%; Pred. No. 1.9e-25;
Matches 139; Conservative 81; Mismatches 191; Indels 364; Gaps 13;
Qy 256 AFQKPVGADVSLGLVPKEELSTQSLPVSGLDPPNCKIDLSPLIDGSTSGKRFRQKOL 315
Db 23 ARERSRGSRISGRHARHPQTALLES---SCENRADLVFIIDSSRVNTHDYAKVKEP 79
Qy 316 LADVAQALDIGPAGPLMGVQVQNDNPATHFNLKHTNSRDLKTAIEKIFQRGSLSNVGA 375
Db 80 IVDILQFLDIGDPVTRVGLLQYGVSTVKNEFSILKTFKRKSEVERAVKRMHLSGTGTGLA 139
Qy 376 ISFTYONPFSKANGN---RSGAPNVVVVWDGWPTDKVBEASRLARESGINIF----- 425
Db 140 IQYALNIAFSEAEAGARPURENVRVIMIVTDGRPODSVAEAAKARDTGILIFAIQGVGV 199
Qy 426 -FITIE--GAENKQYVVEPNF----- 445
Db 200 DFNTLKSIGSEPHEDHVLVAFNSQIETLTSVFQKCLTAHMCSTLEHCAHFCINIPGS 259
Qy 446 -----ANKAVCR----- 452
Db 260 YVCRCKQGYILNSDQTTCTRIQDLCAEDHNCBQLCVNVPSPVCCYGYALAEDEKRCV 319
Qy 453 -----TNGFYSLHVQSWFGL----- 467

Db 320 AVDYCASNHGCEHCENADSGSYLCOCHGEPALNPDEKTCRINYCALNKPGECHBCVNM 379
Qy 468 -----HK--TLQP-----LV-----475
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Db 380 EESYCRCHRGYTLDPNGKTCRDVHCAQDHGCEQLCLNTEDSFVQCQSGFLNEDLK 439
|: ||| |
Qy 476 -----475
Db 440 TCSRVDYCLLDHSGCEYSVNMDSRFACQPEGHVLRSDGKTCALDSCALGDHGCHEHC 499
Qy 476 -----475
Db 500 VSSDSFVQCQPEGYLARBCKTCRDKVCOAIDHGCEHICVNSDDSYTCCLBGFRLAE 559
Qy 476 -----KRVCDTDLACSKTCLNSA-----DIGFVI 500
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Db 560 DGRCRKRDVCKSTHSGCEHICVNNGSYICKSGFVLAEGRCKCKCTEGPIDLVFI 619
Qy 501 DGSSVGTGNRTVLQFVNTLTKPEISDTRIGANVOYTYEORLEPGFDKYSSKPDILN 560
|: ||| |
Db 620 DGSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFLRNFNSAKDMKK 679
Qy 561 AIKRVGYWSGCTSGAAINFALQLEFKK---SKPKRKL---MILITDGRSYDDVRIPAM 614
|: ||| |
Db 680 AVAMKTMKGSMTGLAKENPERSFTQCBGAPLSTVRPRAALVFTDGRAQDDVSEWAS 739
Qy 615 AAHLKGVTITYAIGVAMAAQEELEVIATHPARDHSPFVDFDNLHQYVPRIIQNIC 669
|: ||| |
Db 740 KAKANGITMYAVGVGKALIEELQETASEPTNKHLFYAEDFMTMDISEKLKKGIC 794

RESULT 13

US-08-897-443-3
; Sequence 3, Application US/08897443
; Patent No. 5981263

GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; APPLICANT: Kaser, Mathew
; TITLE OF INVENTION: HUMAN MATRILIN-3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897.443
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PR-0348 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 956 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 2072792
; US-08-897-443-3

Query Match 9.6%; Score 337.5; DB 2; Length 956;

Best Local Similarity 17.4%; Pred. No. 2.3e-22;
Matches 140; Conservative 75; Mismatches 177; Indels 413; Gaps 14;

Qy 269 LVPKEBLSTQLEPVSIGDPNCKIDLSFLIDGSTSIGKRRFRIOKQLADVAQALDIGPA 328
|: ||| |
Db 40 MYPQTALLESC-----NKRADLVFIIDSSRSVNTYDYAKVKEPILDILOFLDIGPD 92
|: ||| |
Qy 329 GPLMGVVOYGNDPATHFLNLTHTNSRDLKTAIEKITORGGLSNVGRALISFVTNPFPSKAN 388
|: ||| |
Db 93 VTRVGLLQYGTGVNPELSKTFKRKSEVERAKRHLSTGTMTGLAIQYALNIAPSEAE 152
|: ||| |
Qy 389 GN---RSGAPNVVVWVGWFTDKVBEASRLAREGINIP-----425
|: ||| |
Db 153 GARPLRENVPRIIMIVTDGRFODSVARVAARNTGILIPAIGVGQVDLNTLKAIGSBPH 212
|: ||| |
Qy 426 -----FITIEG-----431
|: ||| |
Db 213 KDHVFLVANFSQIESLTSVFQNKLCVHSCVLEHCAHFCLTPGSIYICKCKQGYILST 272
|: ||| |
Qy 432 -----AAEN-----435
|: ||| |
Db 273 DQKTCRIQDLCAEDHGCQELCVNMLGSFVQCQSYTLAEDGKRCRTANDYCASENHGCE 332
|: ||| |
Qy 436 -----EKQYVVE-----PNPANKAVCR-----452
|: ||| |
Db 333 HECVNAESSYLRCHEGFPALNSDKTKCKIDYCASNNHCQHECVNAQTSALCRCLKGM 392
|: ||| |
Qy 453 -----452
Db 393 LNPDKTCRINYCALNKPGECHBCVNTBEGHYCHCRQGYNLDPNGKTCRSDVHCAQDQH 452
|: ||| |
Qy 453 -----TNGP-----YSL-----459
|: ||| |
Db 453 GCEQLCLNTEESFVQCQSEGLINDDLTKSRADYCLLSNHCRTYSCVNTDKSPACQCPB 512
|: ||| |
Qy 460 -HVQSWPGLHKTLOPL-----474
|: ||| |
Db 513 GHLVRSQG--KTCAKLDSCALGDHGCHEHSCVSSSEDSFVQCQPEGYLIRDGKTCRDKVC 570
|: ||| |
Qy 475 -----VRRVCDTDLACSKTCLNSA-----494
|: ||| |
Db 571 QDVNHCHEHLCVNSGESYVCKLEGFLAEADGKCRKRNCKSTQHGCEHCVNNGSVL 630
|: ||| |
Qy 495 -----DIGFVIDGSSVGTGNFNTVLQFVNTLKEPISDT 530
|: ||| |
Db 631 CRCSEGFVLAEDGKHCKRCKTEGPIDLVFVFDGSKSLGEENPETVRFVVTGIIDSLAVSPK 690
|: ||| |
Qy 531 DTRIGAVOYTYEORLEPGFDKYSSKPDILNATKRVGWSGGTSTGAAINPALBOLPKSK 590
|: ||| |
Db 691 AARVGLLQYSTQVTEFTLRGFSKAKEMKAVTHMKYKGSMTGLAKHMFERSFTQVE 750
|: ||| |
Qy 591 ----PNKR--KLMILITDGRSYDDVRIPAMAAHLKGVTITYAIGVAMAAQEELEVIATHPA 644
|: ||| |
Db 751 GARPESTQVPRVALVFTDGRAQDDVSEWASAKANGITMYAVGVGKALIEELQETASEPTNKHL 810
|: ||| |
Qy 645 RDHSFFVDFDNLHQYVPRIIQNIC 669
|: ||| |
Db 811 DKHLFYAEDFMTMDISEKLKKGIC 835

RESULT 14

US-08-347-594A-2
; Sequence 2, Application US/08347594A
; Patent No. 5849536
; GENERAL INFORMATION:
; APPLICANT: Garfinkel, Leonard

```
APPLICANT: Richter, Tamar
TITLE OF INVENTION: CLONING AND PRODUCTION OF HUMAN VOM
TITLE OF INVENTION: WILLEBRAND FACTOR GPID BINDING DOMAIN POLYPEPTIDES AND
TITLE OF INVENTION: METHODS OF USING SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,594A
FILING DATE: No. 5849536member 30, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36537-B2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2050 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-347-594A-2

Query Match 7.6%; Score 266; DB 2; Length 2050;
Best Local Similarity 21.9%; Pred. No. 4.6e-15;
Matches 102; Conservative 85; Mismatches 200; Indels 78; Gaps 19;

QY 250 QDPGAAFPKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCK--IDLSELDGSTSIGR 307
DB 475 QEPGLV--PPTDAPVSPPTLYVEDIS----EP-PLHDFYCSRLDLVFLDGGSSRLSEA 528
QY 308 RFRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATFNKLTHTNSRDLKTAIEKITQ 367
DB 529 EFEVLKAPVVDMMERLRIQKWRVAVVEYHDGSHAYIGLKORRPSRLRIASQVKYAG 588
QY 368 G-LSNVGRAISFVTKNFFSKANGRSGAPNVVVMVDGMPDVKVEASRLARESGINIFP 426
DB 589 SQVASTSEVLKYTLFQIFSKI--DRPEASRIALLMAS-----QEPQMSRN----FV 635
QY 427 ITTEGAARENEKQYVVEP-----NPAKAVCRKTNGFYSLHVSQWFLGHLKTLQPL 474
DB 636 RYVQGL--KKKKVIVIPVGIGPHANLQIRLIEKQAPENKAPVLSVDE---LEQQRDEI 690
QY 475 VKRVCDTDLRLACSKTC-----LNS--ADIGFVIDGSSSVGTGN 510
DB 691 VSYLCDLAPAPPTLPDPMAQVTVGPGLLGVSTLGPKNRSMWLDVAFVLEGSXIGRAD 750
QY 511 FRTVLPQVTKLTKFEISDTRIGAVQYTYEORLEFGFDKYSSKPDILNAIKRVGYWSG 570
DB 751 FNRSKFPMEEVIQRMVDVQDSIHVTVLQYSYMTVVEYFPFSAQSGKDILQVRREIRYQGG 810
QY 571 G-TSTGAALNFALEQLFKSKPKNRK---LMILITDGRSYDDV-RIPAMAAHLKGVTYA 625
DB 811 NRTNTGLALRYLSHSLVSGDREQAPNLVYMTGNPASDEIKELPG-----DIQVVP 864
QY 626 IGVAWAAQ-BELEVIAHPARDHSFFVDEDFONLHQYVPRIIQNIC 669
DB 865 IGUGPNANVQELERIGWENPNA---PILIQDFETLPREADPLVLQRC 906
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RESULT 15
US-09-381-261A-1
; Sequence 1, Application US/09381261A
; Patent No. 6489290
; GENERAL INFORMATION:
; APPLICANT: Loscalzo, Joseph
; APPLICANT: Imbal, Aida
; TITLE OF INVENTION: No. 6489290el Anti-Platelet Agent
; FILE REFERENCE: 102258.327
; CURRENT APPLICATION NUMBER: US/09/381.261A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: PCT/US98/06092
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/046,981
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2813
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-381-261A-1

Query Match 7.6%; Score 266; DB 4; Length 2813;
Best Local Similarity 21.9%; Pred. No. 7.9e-15;
Matches 102; Conservative 85; Mismatches 200; Indels 78; Gaps 19;

QY 250 QDPGAAFPKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCK--IDLSELDGSTSIGR 307
DB 1238 QEPGLV--PPTDAPVSPPTLYVEDIS----EP-PLHDFYCSRLDLVFLDGGSSRLSEA 1291
QY 308 RFRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATFNKLTHTNSRDLKTAIEKITQ 367
DB 1292 EFEVLKAPVVDMMERLRIQKWRVAVVEYHDGSHAYIGLKORRPSRLRIASQVKYAG 1351
QY 368 G-LSNVGRAISFVTKNFFSKANGRSGAPNVVVMVDGMPDVKVEASRLARESGINIFP 426
DB 1352 SQVASTSEVLKYTLFQIFSKI--DRPEASRIALLMAS-----QEPQMSRN----FV 1398
QY 427 ITTEGAARENEKQYVVEP-----NPAKAVCRKTNGFYSLHVSQWFLGHLKTLQPL 474
DB 1399 RYVQGL--KKKKVIVIPVGIGPHANLQIRLIEKQAPENKAPVLSVDE---LEQQRDEI 1453
QY 475 VKRVCDTDLRLACSKTC-----LNS--ADIGFVIDGSSSVGTGN 510
DB 1454 VSYLCDLAPAPPTLPDPMAQVTVGPGLLGVSTLGPKNRSMWLDVAFVLEGSXIGRAD 1513
QY 511 FRTVLPQVTKLTKFEISDTRIGAVQYTYEORLEFGFDKYSSKPDILNAIKRVGYWSG 570
DB 1514 FNRSKFPMEEVIQRMVDVQDSIHVTVLQYSYMTVVEYFPFSAQSGKDILQVRREIRYQGG 1573
QY 571 G-TSTGAALNFALEQLFKSKPKNRK---LMILITDGRSYDDV-RIPAMAAHLKGVTYA 625
DB 1574 NRTNTGLALRYLSHSLVSGDREQAPNLVYMTGNPASDEIKELPG-----DIQVVP 1627
QY 626 IGVAWAAQ-BELEVIAHPARDHSFFVDEDFONLHQYVPRIIQNIC 669
DB 1628 IGUGPNANVQELERIGWENPNA---PILIQDFETLPREADPLVLQRC 1669
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Job time : 48 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 16:44:54 ; Search time 48 Seconds
(without alignments)
3944.399 Million cell updates/sec

Title: US-10-063-688-34

Perfect score: 3502
Sequence: 1 MRTVLTWKSASVIEFLVLL.....QYPRITQICTEFTNSQPN 678

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	3502	100.0	678	9	US-09-989-723-179
6	3502	100.0	678	9	US-09-989-723-179
7	3502	100.0	678	9	US-09-989-723-179
8	3502	100.0	678	9	US-09-989-723-179
9	3502	100.0	678	9	US-09-989-723-179
10	3502	100.0	678	9	US-09-989-723-179
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16	3502	100.0	678	9	US-09-990-444-179
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18	3502	100.0	678	9	US-09-989-730-179
19	3502	100.0	678	9	US-09-990-436-179
20	3502	100.0	678	9	US-09-993-687-179
21	3502	100.0	678	10	US-09-989-734-179
22	3502	100.0	678	10	US-09-997-653-179
23	3502	100.0	678	10	US-09-993-667-179
24	3502	100.0	678	10	US-09-997-428-179
25	3502	100.0	678	10	US-09-997-666-179
26	3502	100.0	678	10	US-09-990-438-179
27	3502	100.0	678	10	US-09-990-562-179
28	3502	100.0	678	10	US-09-990-711-179
29	3502	100.0	678	10	US-09-989-726-179
30	3502	100.0	678	10	US-09-998-156-179
31	3502	100.0	678	10	US-09-990-437-179
32	3502	100.0	678	10	US-09-991-157-179
33	3502	100.0	678	10	US-09-997-514-179
34	3502	100.0	678	10	US-09-997-573-179
35	3502	100.0	678	10	US-09-991-172-179
36	3502	100.0	678	10	US-09-990-726-179
37	3502	100.0	678	10	US-09-997-559-179
38	3502	100.0	678	10	US-09-997-601-179
39	3502	100.0	678	10	US-09-990-443-179
40	3502	100.0	678	10	US-09-991-854-179
41	3502	100.0	678	10	US-09-997-628-179
42	3502	100.0	678	10	US-09-997-683-179
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ALIGNMENTS

RESULT 1

US-09-989-722-179

; Sequence 179, Application US/09989722

; Patent No. US20020072067A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730PIC63

; CURRENT APPLICATION NUMBER: US/09/989,722

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1 PRIOR APPLICATION NUMBER: 60/065186
2 PRIOR FILING DATE: 1997-11-12
3 PRIOR APPLICATION NUMBER: 60/065311
4 PRIOR FILING DATE: 1997-11-13
5 PRIOR APPLICATION NUMBER: 60/066770
6 PRIOR FILING DATE: 1997-11-24
7 PRIOR APPLICATION NUMBER: 60/075945
8 PRIOR FILING DATE: 1998-02-25
9 PRIOR APPLICATION NUMBER: 60/078910
10 PRIOR FILING DATE: 1998-03-20
11 PRIOR APPLICATION NUMBER: 60/083322
12 PRIOR FILING DATE: 1998-04-28
13 PRIOR APPLICATION NUMBER: 60/084600
14 PRIOR FILING DATE: 1998-05-07
15 PRIOR APPLICATION NUMBER: 60/087106
16 PRIOR FILING DATE: 1998-05-28
17 PRIOR APPLICATION NUMBER: 60/087607
18 PRIOR FILING DATE: 1998-06-02
19 PRIOR APPLICATION NUMBER: 60/087609
20 PRIOR FILING DATE: 1998-06-02
21 PRIOR APPLICATION NUMBER: 60/087759
22 PRIOR FILING DATE: 1998-06-02
23 PRIOR APPLICATION NUMBER: 60/087827
24 PRIOR FILING DATE: 1998-06-03
25 PRIOR APPLICATION NUMBER: 60/088021
26 PRIOR FILING DATE: 1998-06-04
27 PRIOR APPLICATION NUMBER: 60/088025
28 PRIOR FILING DATE: 1998-06-04
29 PRIOR APPLICATION NUMBER: 60/088026
30 PRIOR FILING DATE: 1998-06-04
31 PRIOR APPLICATION NUMBER: 60/088028
32 PRIOR FILING DATE: 1998-06-04
33 PRIOR APPLICATION NUMBER: 60/088029
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35 PRIOR APPLICATION NUMBER: 60/088030
36 PRIOR FILING DATE: 1998-06-04
37 PRIOR APPLICATION NUMBER: 60/088033
38 PRIOR FILING DATE: 1998-06-04
39 PRIOR APPLICATION NUMBER: 60/088326
40 PRIOR FILING DATE: 1998-06-04
41 PRIOR APPLICATION NUMBER: 60/088167
42 PRIOR FILING DATE: 1998-06-05
43 PRIOR APPLICATION NUMBER: 60/088202
44 PRIOR FILING DATE: 1998-06-05
45 PRIOR APPLICATION NUMBER: 60/088212
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47 PRIOR APPLICATION NUMBER: 60/088217
48 PRIOR FILING DATE: 1998-06-05
49 PRIOR APPLICATION NUMBER: 60/088655
50 PRIOR FILING DATE: 1998-06-09
51 PRIOR APPLICATION NUMBER: 60/088734
52 PRIOR FILING DATE: 1998-06-10
53 PRIOR APPLICATION NUMBER: 60/088738
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55 PRIOR APPLICATION NUMBER: 60/088742
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63 PRIOR APPLICATION NUMBER: 60/088858
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65 PRIOR APPLICATION NUMBER: 60/088861
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69 PRIOR APPLICATION NUMBER: 60/089105
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;; PRIOR APPLICATION NUMBER: 60/091360
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;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.7e-293; Indels 0; Gaps 0;
Matches 678; Conservative 0; Mismatches 0;

Qy	1	MRTVLTWKASVEMFLVLLVTGHSNKTAKIKRPKFTVPQINCDVKGKIIDPPIV	60
Db	1	MRTVLTWKASVEMFLVLLVTGHSNKTAKIKRPKFTVPQINCDVKGKIIDPPIV	60
Qy	61	KCPAGCQDPKYHVYGTVDVYASVYCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG	120
Db	61	KCPAGCQDPKYHVYGTVDVYASVYCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG	120
Qy	121	VQSLSLPRWRESPIVLSKPKKGTVPYSAITYSSKSPAAQAGETTKAYQRPPIGTTAQ	180
Db	121	VQSLSLPRWRESPIVLSKPKKGTVPYSAITYSSKSPAAQAGETTKAYQRPPIGTTAQ	180
Qy	181	PVTLMQLLAVTVATPTTLPRPSPSAATTSIPRQSVGHRQBMDLWSTATTSSQNR	240
Db	181	PVTLMQLLAVTVATPTTLPRPSPSAATTSIPRQSVGHRQBMDLWSTATTSSQNR	240
Qy	241	PRADPGIORQDPGSAAGFKPVGADVSLGLVPKEELSTQSLPVSIGDPNCKIDLSPLIDG	300
Db	241	PRADPGIORQDPGSAAGFKPVGADVSLGLVPKEELSTQSLPVSIGDPNCKIDLSPLIDG	300
Qy	301	STSIGKRRFRIQKOLLADVAQALDIPAGPLMGVYVQYGDNPATPHNLKHTNSRDLKTAI	360
Db	301	STSIGKRRFRIQKOLLADVAQALDIPAGPLMGVYVQYGDNPATPHNLKHTNSRDLKTAI	360
Qy	361	EKITQRCGLSNVGRASIVFTYKNFFSKANGNSGAPNVMVWDGNPTDKVEASRLARES	420
Db	361	EKITQRCGLSNVGRASIVFTYKNFFSKANGNSGAPNVMVWDGNPTDKVEASRLARES	420
Qy	421	GINIFFITIEGAENKQYVVEPNFANKAVCTRTNGFYSLHVQSWFGLHKTLPVLRVCD	480
Db	421	GINIFFITIEGAENKQYVVEPNFANKAVCTRTNGFYSLHVQSWFGLHKTLPVLRVCD	480
Qy	481	TDLACSKTCLNSADIGFVINDGSSVGTGNFTVLQFVTNLTKFPISTDTTRIGAVQYT	540
Db	481	TDLACSKTCLNSADIGFVINDGSSVGTGNFTVLQFVTNLTKFPISTDTTRIGAVQYT	540
Qy	541	YEORLEFGFDKYSKPDILNAIKRVGYWSGCTGTGAALNPALEQLFKKSKENKCKMLLI	600
Db	541	YEORLEFGFDKYSKPDILNAIKRVGYWSGCTGTGAALNPALEQLFKKSKENKCKMLLI	600
Qy	601	TGGRSYDDVRIPAMAHLKGVITTAIGVAAQAQBELEVIATPHARDHSFFVDBEDNLHQY	660
Db	601	TGGRSYDDVRIPAMAHLKGVITTAIGVAAQAQBELEVIATPHARDHSFFVDBEDNLHQY	660
Qy	661	VPRIIQICTEFNSQPRN 678	
Db	661	VPRIIQICTEFNSQPRN 678	

RESULT 2

US-09-989-723-179
; Sequence 179, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Paoni, Nicholas P.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTVLTWKASVTEMFLVTLVTVGVHNSKETAACKIKRPFVTPQINCDVKAGKIIDPEFIV 60
Db 1 MRTVLTWKASVTEMFLVTLVTVGVHNSKETAACKIKRPFVTPQINCDVKAGKIIDPEFIV 60
Qy 61 KCPAGCQDPKYHVYGTVDVYASYSVCGAAVHSGVLDNSGGKILVRKAVAGQSGYKGSYNG 120
Db 61 KCPAGCQDPKYHVYGTVDVYASYSVCGAAVHSGVLDNSGGKILVRKAVAGQSGYKGSYNG 120
Qy 121 VQSLSLPRWRRESFIVLESKPKKGTYPYTSALTYSSSKSPAAQAGETTKAYQRPPIRGTTAQ 180
Db 121 VQSLSLPRWRRESFIVLESKPKKGTYPYTSALTYSSSKSPAAQAGETTKAYQRPPIRGTTAQ 180
Qy 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTISIIPQSVGHRSQBMDLWSTATYTTSQNR 240
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Db 181 PVTLLQLLAVTAVATPTLPRPSPSAATSTISPRPQSVGRSOPQDLWSTATTYSSQNR 240
Qy 241 PRADPGIORQDPGSAAGFKPGADVSLGLVPRKEELSTQSLPVSIGDPNCKDLSFLIDG 300
Db 241 PRADPGIORQDPGSAAGFKPGADVSLGLVPRKEELSTQSLPVSIGDPNCKDLSFLIDG 300
Qy 301 STSIGKRFRIOKOLLADVAQALDIGPAGPLMGVVQYGDNPATPHNLKTHNTSRDLKTAI 360
Db 301 STSIGKRFRIOKOLLADVAQALDIGPAGPLMGVVQYGDNPATPHNLKTHNTSRDLKTAI 360
Qy 361 EKITQGGLSNVGRAISFVTKNFTSKANGNSGAPNVVVWVGWPTDKVEEASRLARES 420
Db 361 EKITQGGLSNVGRAISFVTKNFTSKANGNSGAPNVVVWVGWPTDKVEEASRLARES 420
Qy 421 GINIFFITIEGAAREKQYVVEPNPANKAVCRKTNGFYSLHVQSWFGLHKTQLPLVKRYCD 480
Db 421 GINIFFITIEGAAREKQYVVEPNPANKAVCRKTNGFYSLHVQSWFGLHKTQLPLVKRYCD 480
Qy 481 TDLRACSKTCLNSADIGFVIDSSVGTGNFRTVLQFVTNLTKBFEISDTRIGAVQYT 540
Db 481 TDLRACSKTCLNSADIGFVIDSSVGTGNFRTVLQFVTNLTKBFEISDTRIGAVQYT 540
Qy 541 YEQRLEFGDKYSKPDILNAIKRVGWSGGTSTGAAINFPALEQLFKSKKPKKRLMILI 600
Db 541 YEQRLEFGDKYSKPDILNAIKRVGWSGGTSTGAAINFPALEQLFKSKKPKKRLMILI 600
Qy 601 TDGSDYDDVRIPAMAHLKGVITTAIGVAMAQEELEVIATHPARDHSFFVDFDNLHQY 660
Db 601 TDGSDYDDVRIPAMAHLKGVITTAIGVAMAQEELEVIATHPARDHSFFVDFDNLHQY 660
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Db 661 VPRIIONICTFNSQPRN 678

RESULT 3
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; Sequence 179, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C36
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
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QY 1 MRTVLTNKAASVIEFLLVTVGVHSNKETAKKIKRPFVTPQINCVDKAGKIIDPEFIV 60
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DB 181 PVTLMQLLAVTVAVATPTTLPRPSPAASATTSIPRQSVGHSQEMDLWSTATYTSQQNR 240

QY 241 PRADPGIORQDPGSGAAFOKPVGADYSLGLVPKEELSTQSLPVSGLDPNCKIDLSPIDG 300
DB 241 PRADPGIORQDPGSGAAFOKPVGADYSLGLVPKEELSTQSLPVSGLDPNCKIDLSPIDG 300

QY 301 STSICKRRFRIOKQLLADVAQALDIPAGPLMGVYQYGDNPATHTNLTNSRDLKTAL 360
DB 301 STSICKRRFRIOKQLLADVAQALDIPAGPLMGVYQYGDNPATHTNLTNSRDLKTAL 360

QY 361 EKITORGGLSNVGRAISFVTKNPFPSKANGNRSGAPNVVVMVDGWPDKVBEASRLARES 420
DB 361 EKITORGGLSNVGRAISFVTKNPFPSKANGNRSGAPNVVVMVDGWPDKVBEASRLARES 420

QY 421 GINIFPITIIEGAANEKQYVVEPNPANKAVCTNGTFYSLHVQSWFGLHKTLOPLVKRVCD 480
DB 421 GINIFPITIIEGAANEKQYVVEPNPANKAVCTNGTFYSLHVQSWFGLHKTLOPLVKRVCD 480

QY 481 TDRLACSKTCLNSADIGFVIDGSSVCGNFTVLOFTNLTKPEISDPTDRIGAVQYT 540
DB 481 TDRLACSKTCLNSADIGFVIDGSSVCGNFTVLOFTNLTKPEISDPTDRIGAVQYT 540

QY 541 YBQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAANFALFQLPKSKPNKRKLMILI 600
DB 541 YBQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAANFALFQLPKSKPNKRKLMILI 600

QY 601 TDGRSYDDVRIPAMAHLKGVITYAIGVAAQAQBELEVIATHPARDHSFVDFDNLHQY 660
DB 601 TDGRSYDDVRIPAMAHLKGVITYAIGVAAQAQBELEVIATHPARDHSFVDFDNLHQY 660

QY 661 VPRITQNTCTEFNSQPRN 678
DB 661 VPRITQNTCTEFNSQPRN 678

RESULT 4

US-989-727-179
; Sequence 179, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1998-02-25
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35	;	PRIOR APPLICATION NUMBER:	60/090862
36	;	PRIOR FILING DATE:	1998-06-25
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53	;	PRIOR APPLICATION NUMBER:	60/091982
54	;	PRIOR FILING DATE:	1998-07-07
55	;	PRIOR APPLICATION NUMBER:	60/092182
56	;	PRIOR FILING DATE:	1998-07-09

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Qy	1	MRTVVLTKGASVTIEMPTLVLLVTGVHSSNKETAAKIKRPKFTVPQINCVDWAGKIIDPPIV	60		
Dd	1	MRTVVLTKGASVTIEMPTLVLLVTGVHSSNKETAAKIKRPKFTVPQINCVDWAGKIIDPPIV	60		
Qy	61	KCPAGCQDPKYHYGTVDVIYASYSSVCCAA VHS GVL D N S G G K I L V R K V A G Q S G Y K G S Y N G	120		
Dd	61	KCPAGCQDPKYHYGTVDVIYASYSSVCCAA VHS GVL D N S G G K I L V R K V A G Q S G Y K G S Y N G	120		
Qy	121	VQSLSLPRWRRESFIVLSKKPKGVTPYSALTYSSSKSPAAQAQGETTXYQRPPITGGTAQ	180		
Dd	121	VQSLSLPRWRRESFIVLSKKPKGVTPYSALTYSSSKSPAAQAQGETTXYQRPPITGGTAQ	180		

Qy	181	PVTLMOLLAVTVA	VATPTTLPRPSPSA	ASTTTS	I	PPROSVGHR	SOBMDL	WSTATYT	SSQNR	240	
Db	181	PVTLMOLLAVTVA	VATPTTLPRPSPSA	ASTTTS	I	PPROSVGHR	SOBMDL	WSTATYT	SSQNR	240	
Qy	241	PRADPGIORQDPS	GAAPQKPGVADVS	LGLVPK	BELS	TQSLEPVS	LGD	PNCKID	LSFLIDG	300	
Db	241	PRADPGIORQDPS	GAAPQKPGVADVS	LGLVPK	BELS	TQSLEPVS	LGD	PNCKID	LSFLIDG	300	
Qy	301	STSTIGKBRPRI	QKOLLADVAQAL	DI	GPAGPLMG	VVQVQ	GDNPAT	HTFN	LKTH	NSRDLKTAI	360
Db	301	STSTIGKBRPRI	QKOLLADVAQAL	DI	GPAGPLMG	VVQVQ	GDNPAT	HTFN	LKTH	NSRDLKTAI	360
Qy	361	EKITQRGGLSNV	GRAISFVTKN	PPSKANGNR	S	GAPNVVV	MVDG	MPTDKV	BEASPLARES	420	
Db	361	EKITQRGGLSNV	GRAISFVTKN	PPSKANGNR	S	GAPNVVV	MVDG	MPTDKV	BEASPLARES	420	
Qy	421	GINIFPTITISGA	ENRKQYVVB	PNPANKA	VCRTNG	PFSLHVQS	WFLG	LKTLQPLV	VRVCD	480	
Db	421	GINIFPTITISGA	ENRKQYVVB	PNPANKA	VCRTNG	PFSLHVQS	WFLG	LKTLQPLV	VRVCD	480	
Qy	481	TDRLACSKTCLNS	ADIGFVIDG	SSSVG	TGNFRTVLQ	PVTNLTK	BEIS	TD	TRIGAVQYT	540	
Db	481	TDRLACSKTCLNS	ADIGFVIDG	SSSVG	TGNFRTVLQ	PVTNLTK	BEIS	TD	TRIGAVQYT	540	
Qy	541	YBQRLRPGFUKY	SKPDILNAI	KRVGYWS	GGTSTG	GA	INFALEOL	FKKS	KENK	KMLIL	600
Db	541	YBQRLRPGFUKY	SKPDILNAI	KRVGYWS	GGTSTG	GA	INFALEOL	FKKS	KENK	KMLIL	600
Qy	601	TDCRSYDDVRI	PAMAHLKGVIT	YIAI	GVAMAAQ	EE	LEVIA	TH	PARDHS	FFVDEPONTLHQY	660
Db	601	TDCRSYDDVRI	PAMAHLKGVIT	YIAI	GVAMAAQ	EE	LEVIA	TH	PARDHS	FFVDEPONTLHQY	660
Qy	661	VPRIIQNICTEF	NSQPN	678							
Db	661	VPRIIQNICTEF	NSQPN	678							

RESULT 5

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US-09-989-731-179
: Sequence 179, Application US/09989731
: Patent No. US20020103125A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730PIC70
: CURRENT APPLICATION NUMBER: US/09/989,731
: CURRENT FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16

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1	PRIOR FILING DATE: 1998-06-16
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5	PRIOR FILING DATE: 1998-06-16
6	PRIOR APPLICATION NUMBER: 60/089532
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22	PRIOR APPLICATION NUMBER: 60/089908
23	PRIOR FILING DATE: 1998-06-18
24	PRIOR APPLICATION NUMBER: 60/089947
25	PRIOR FILING DATE: 1998-06-19
26	PRIOR APPLICATION NUMBER: 60/089948
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28	PRIOR APPLICATION NUMBER: 60/089952
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73	PRIOR FILING DATE: 1998-06-26

;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
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;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;

Best Local Similarity 100.0%; Pred No. 1.7e-293;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 VQSLSPRRRESFVLESKPKGKGVTPSALTYSSKSPAAQAGETTKAYORPIPGTTAQ 180
DB 121 VQSLSPRRRESFVLESKPKGKGVTPSALTYSSKSPAAQAGETTKAYORPIPGTTAQ 180
QY 181 PVTLMOLLAVTVAVTPTTLPRPSPSAASTTSIPRQSVGHRSGQMDLMSATYTSQNR 240
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RESULT 6

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; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyere, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary B.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.7e-293; Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 KCPAGCQDPKTHVGTGTDVYASYSYCGAAVHSGVLDNSGKILVRKVAQSGYKGSYSNG 120

Qy 121 VQSLSLPRWRESFIVLESKPKKGVTPSALTYSYSSKSPAAQAGETTAKYORPPIPTTAAQ 180

Db 121 VQSLSLPRWRESFIVLESKPKKGVTPSALTYSYSSKSPAAQAGETTAKYORPPIPTTAAQ 180

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QY 241 PRADPGIQRDPGSAFQKPVGADVSLGLVPKKELSQSLPVSLSGDPNCKIDLSPLIDG 300
DB 241 PRADPGIQRDPGSAFQKPVGADVSLGLVPKKELSQSLPVSLSGDPNCKIDLSPLIDG 300
QY 301 STSIGKRRFRIQKQLADVAQALDIGPAGPLMGVVQYCDNPNATHFNKLTHTNSRDLKTAI 360
DB 301 STSIGKRRFRIQKQLADVAQALDIGPAGPLMGVVQYCDNPNATHFNKLTHTNSRDLKTAI 360
QY 361 EKITQRGLSNVGRRAISFVTKNFPFSKANGRSGAPNVVVMVDCGWPTDKVEEASRLARES 420
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QY 421 GINIFPITIIEGAENEKOYVVEPFAKNCRTNGFYSLHVQSWFGLHKTLOPLVKRVCD 480
DB 421 GINIFPITIIEGAENEKOYVVEPFAKNCRTNGFYSLHVQSWFGLHKTLOPLVKRVCD 480
QY 481 TDLRACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTIRIGAVQYT 540
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DB 661 VPRIIQCITFEFNSQPN 678

RESULT 7
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; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
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Db 361 EKITQRCGLSNVGRAISFVTITNPFSSKANGNRSGAPNVVVVVDGWPTDKVBEASRLARES 420

Qy 421 GINIFFITIEGAENKQYVVEPNFANKAVCTRTNGFYSLHVQSWFGLHKTLOPLVKRUCD 480
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Db 661 VPRIIQNICTEFNSQPRN 678

RESULT 8
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: Patent No. US20020132252A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
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: APPLICANT: Matanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2730P1C8
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73	PRIOR FILING DATE: 1998-06-25	

Db 561 VPRIQNICTEFNSQPRN 678
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 ; Sequence 179, Application US/09993604
 ; Patent No. US20020137075A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deanoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Kurney, Austin L.
 ; APPLICANT: Kujavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
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 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Tutanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Acids Encoding
 ; FILE REFERENCE: P2730P1C25
 ; CURRENT APPLICATION NUMBER: US/09/99
 ; CURRENT FILING DATE: 2001-11-14
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
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Matches 678; Conservative 0; Mismatches 0;

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Qy 121 VQSLPFRWRESFIVLESKPKGGVTPSALTYSSSKSPAQAQAGTTKAYQRPPIPTTTAQ 180

Db 121 VQSLSLPRWRSFVLESKPKRGVTPSALTYSKSPAAQAGETTKAYQRPPIPGTTAQ 180
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Db 181 PVTLMQLLAVTAVATPTTLPRPSPSAASTTISIPRPSQVGHRSQBMDLWSTATTYSSQNR 240
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Db 241 PRADPGIORQPSGAPKQPGADVSLGLVPEKHELSTQSLPVSIGDPCNKIDLSFLIDG 300
Qy 301 STSIGKRFRIOKOLLADVAQALDIGPAGPLMGVVQYGDNPATPHNLKHTNSRDLKTAI 360
Db 301 STSIGKRFRIOKOLLADVAQALDIGPAGPLMGVVQYGDNPATPHNLKHTNSRDLKTAI 360
Qy 361 EKITORGLSNVGRAISFVTKNPFKSKANGRSAGPNVVMVDGWPPTDKVEEASRLARES 420
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; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; FILE REFERENCE: P2730PIC22
; CURRENT APPLICATION NUMBER: US/09/990,456

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Query Match 100.0%; Score 3502; DB 9; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.7e-293; Mismatches 0; Indels 0; Gaps 0;
Matches 678; Conservative 0;

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Qy 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTISIPRQSVGHRSQEMDLWSTATTYTSSQNR 240
Db 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTISIPRQSVGHRSQEMDLWSTATTYTSSQNR 240
Qy 241 PRADPGIORQDPGSGAAGFQKPVGADVSLGLVPKHELSTQSLPVSIGDPNCKIDLSFLIDG 300
Db 241 PRADPGIORQDPGSGAAGFQKPVGADVSLGLVPKHELSTQSLPVSIGDPNCKIDLSFLIDG 300
Qy 301 STSIGKRFRFRIQKQLLADVAQALDIPAGPLMGVVOYGDNPATFNLTHTNSRDLKTAI 360
Db 301 STSIGKRFRFRIQKQLLADVAQALDIPAGPLMGVVOYGDNPATFNLTHTNSRDLKTAI 360
Qy 361 EKITORGGLSNVGRASIFVTNPFKANGNSGAPNVVVMVDGWFTDKVBEASRLARES 420
Db 361 EKITORGGLSNVGRASIFVTNPFKANGNSGAPNVVVMVDGWFTDKVBEASRLARES 420
Qy 421 GINIPTITIEGAAENKQYVVEPNPANKAVCKTNGTFYSLHVQSWFGLHKTLPVKRVC 480
Db 421 GINIPTITIEGAAENKQYVVEPNPANKAVCKTNGTFYSLHVQSWFGLHKTLPVKRVC 480
Qy 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFTVLQFVTNLTKBPEISDTRIGAVQVT 540
Db 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFTVLQFVTNLTKBPEISDTRIGAVQVT 540
Qy 541 YEQRLEFGFDKYSSKPDILNAIKRQVYNSGGTSTGAAINFALQPLPKSKPNKRKLMI 600
Db 541 YEQRLEFGFDKYSSKPDILNAIKRQVYNSGGTSTGAAINFALQPLPKSKPNKRKLMI 600
Qy 601 TDGRSYDDVRIPAMAAHLKGVITYAIGVAAQAQBELEVIAHPARDHSFPVDFNLHQY 660
Db 601 TDGRSYDDVRIPAMAAHLKGVITYAIGVAAQAQBELEVIAHPARDHSFPVDFNLHQY 660
Qy 661 VPRIIQNICTEFNSQPRN 678

Db 661 VPRIIQICTEFSQPN 678

RESULT 12

US-09-989-721-179

Sequence 179, Application US/09989721

Patent No. US20020142961A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

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APPLICANT: Eaton, Dan L.

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APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: KJavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE REFERENCE: P2730PIC55

CURRENT APPLICATION NUMBER: US/09/989,721

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

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PRIOR FILING DATE: 1998-06-19

PRIOR APPLICATION NUMBER: 60/090246

PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: 60/090252

PRIOR FILING DATE: 1998-06-22

Prior Application Number: 60/090254
Prior Filing Date: 1998-06-22
Prior Application Number: 60/090349
Prior Filing Date: 1998-06-23
Prior Application Number: 60/090355
Prior Filing Date: 1998-06-23
Prior Application Number: 60/090429
Prior Filing Date: 1998-06-24
Prior Application Number: 60/090431
Prior Filing Date: 1998-06-24
Prior Application Number: 60/090435
Prior Filing Date: 1998-06-24
Prior Application Number: 60/090444
Prior Filing Date: 1998-06-24
Prior Application Number: 60/090445
Prior Filing Date: 1998-06-24
Prior Application Number: 60/090472
Prior Filing Date: 1998-06-24
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Prior Filing Date: 1998-06-26
Prior Application Number: 60/090863
Prior Filing Date: 1998-06-26
Prior Application Number: 60/091360
Prior Filing Date: 1998-07-01
Prior Application Number: 60/091478
Prior Filing Date: 1998-07-02
Prior Application Number: 60/091544
Prior Filing Date: 1998-07-01
Prior Application Number: 60/091519
Prior Filing Date: 1998-07-02
Prior Application Number: 60/091626
Prior Filing Date: 1998-07-02
Prior Application Number: 60/091633
Prior Filing Date: 1998-07-02
Prior Application Number: 60/091978
Prior Filing Date: 1998-07-07
Prior Application Number: 60/091982
Prior Filing Date: 1998-07-07
Prior Application Number: 60/092182
Prior Filing Date: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRTVLTWKAASVEMFLVLTGHSNKEAKKIKRPFVTPQINCVDKAGKIIDPEFIV 60

Qy 61 KCPAGODPKYHYVGTVDYASVSCGAAVHSGVLDNSGKILVRKVGAGSGYKGSYNG 120
Db 61 KCPAGODPKYHYVGTVDYASVSCGAAVHSGVLDNSGKILVRKVGAGSGYKGSYNG 120

RESULT 13
US-09-992-598-179
Sequence 179, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Pong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCES: P2730P1C20

[illegible]

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2 PRIOR FILING DATE: 1998-06-25
3 PRIOR APPLICATION NUMBER: 60/090862
4 PRIOR FILING DATE: 1998-06-26
5 PRIOR APPLICATION NUMBER: 60/090863
6 PRIOR FILING DATE: 1998-06-26
7 PRIOR APPLICATION NUMBER: 60/091360
8 PRIOR FILING DATE: 1998-07-01
9 PRIOR APPLICATION NUMBER: 60/091478
10 PRIOR FILING DATE: 1998-07-02
11 PRIOR APPLICATION NUMBER: 60/091544
12 PRIOR FILING DATE: 1998-07-01
13 PRIOR APPLICATION NUMBER: 60/091519
14 PRIOR FILING DATE: 1998-07-02
15 PRIOR APPLICATION NUMBER: 60/091626
16 PRIOR FILING DATE: 1998-07-02
17 PRIOR APPLICATION NUMBER: 60/091633
18 PRIOR FILING DATE: 1998-07-02
19 PRIOR APPLICATION NUMBER: 60/091978
20 PRIOR FILING DATE: 1998-07-07
21 PRIOR APPLICATION NUMBER: 60/091982
22 PRIOR FILING DATE: 1998-07-07
23 PRIOR APPLICATION NUMBER: 60/092182
24 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 M R T V L T M K A S V T E M F L V L L V T G V H S N K E T A K K I R K P F T V P Q I N C D V K A G K I D P E F I V 60
Qy 61 K C P A G C Q D P K H V G T D V I A S Y S V C C A A V H S G V L D N S G G K I L V R K V A G S G Y K G S Y S N G 120
Db 61 K C P A G C Q D P K H V G T D V I A S Y S V C C A A V H S G V L D N S G G K I L V R K V A G S G Y K G S Y S N G 120
Qy 121 V Q S L S L P R W R E S F T V L S K P K G V T Y P S A L T Y S S K S P A A Q A G E T T K A Y O R P P I P G T T A Q 180
Db 121 V Q S L S L P R W R E S F T V L S K P K G V T Y P S A L T Y S S K S P A A Q A G E T T K A Y O R P P I P G T T A Q 180
Qy 181 P V T L M Q L L A V T A V A T P T L P R P S P S A A T T S I P R P Q S V G H R S Q E M D L W S T A T T Y S S Q N R 240
Db 181 P V T L M Q L L A V T A V A T P T L P R P S P S A A T T S I P R P Q S V G H R S Q E M D L W S T A T T Y S S Q N R 240
Qy 241 P R A D P G I Q R O D P S G A A F Q K P V G A D V S L G L V P K E E L S T Q S L E P V S L G D P N C K I D L S F L I D G 300
Db 241 P R A D P G I Q R O D P S G A A F Q K P V G A D V S L G L V P K E E L S T Q S L E P V S L G D P N C K I D L S F L I D G 300
Qy 301 S T S I G K R R F R I Q K O L L A D V A Q A L D I G P A G P L M G V V Q Y G D N P A T H F N L K T H T N S R D L K T A I 360
Db 301 S T S I G K R R F R I Q K O L L A D V A Q A L D I G P A G P L M G V V Q Y G D N P A T H F N L K T H T N S R D L K T A I 360
Qy 361 E K I T O R G L S N V G R A I S F V T K N P F S K A N G R S G A P N V V W V D G W P T D K V E A S R L A R E S 420
Db 361 E K I T O R G L S N V G R A I S F V T K N P F S K A N G R S G A P N V V W V D G W P T D K V E A S R L A R E S 420
Qy 421 G I N I F P T I T E G A A N E K Q V V E P F A N K A V C R T N G F Y S L H V Q S F L G L K T L Q P L V K E V C D 480
Db 421 G I N I F P T I T E G A A N E K Q V V E P F A N K A V C R T N G F Y S L H V Q S F L G L K T L Q P L V K E V C D 480
Qy 481 T D R L A C S K T C L N S A D I G F V I D G S S V G T G N F R T V L Q F V T N L T K E F E I S D T D T R I G A V O Y T 540
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Qy 541 Y E Q L E R F G F D K Y S K P D I L N A I K R V G Y S G T S T G A I N F A L E Q L P K K S P N K K M I L I 600
Db 541 Y E Q L E R F G F D K Y S K P D I L N A I K R V G Y S G T S T G A I N F A L E Q L P K K S P N K K M I L I 600
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RESULT 14
US-09-989-293A-179
; Sequence 179, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Garber, Hanspeter
; APPLICANT: Gottard, Audrey E.
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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43	PRIOR FILING DATE: 1998-06-26	
44	PRIOR APPLICATION NUMBER: 60/091360	
45	PRIOR FILING DATE: 1998-07-01	
46	PRIOR APPLICATION NUMBER: 60/091478	
47	PRIOR FILING DATE: 1998-07-02	
48	PRIOR APPLICATION NUMBER: 60/091544	
49	PRIOR FILING DATE: 1998-07-01	
50	PRIOR APPLICATION NUMBER: 60/091519	
51	PRIOR FILING DATE: 1998-07-02	
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56	PRIOR APPLICATION NUMBER: 60/091978	
57	PRIOR FILING DATE: 1998-07-07	
58	PRIOR APPLICATION NUMBER: 60/091982	
59	PRIOR FILING DATE: 1998-07-07	
60	PRIOR APPLICATION NUMBER: 60/092182	
61	PRIOR FILING DATE: 1998-07-09	

Query Match	100.0%	Score 3502;	DB 9;	Length 678;
Best Local Similarity	100.0%	Pred. NO. 1.7e-293;		
Matches 678;	Conservative 0;	Mismatches 0;	Indels 0;	

Qy	1	MRTVVLTKKASVTEMPLVLLVTGVSHNKETA	KIKPKFTVPQINCDVKA	KGIKIDPEFIV	60
Db	1	MRTVVLTKKASVTEMPLVLLVTGVSHNKETA	KIKPKFTVPQINCDVKA	KGIKIDPEFIV	60
Qy	61	KCPAGQCDPKHYVGTDDVYASSVCGAAVHSG	VLDSGGKILVRKVA	QSGYKGSYSG	120
Db	61	KCPAGQCDPKHYVGTDDVYASSVCGAAVHSG	VLDSGGKILVRKVA	QSGYKGSYSG	120

121 VOSLSLPRWRESFVLESKPKGVTPSALTYSSSKSPAAQAGETTKAYORPPIGTTAQ 180
121 VQSLSLPRWRESFVLESKPKGVTPSALTYSSSKSPAAQAGETTKAYORPPIGTTAQ 180
181 PVTLMQLLAVTVATPTTLPRPSPAASTTSIPRPSQVGHRSQEMDLNSTATYTSQNR 240
181 PVTLMQLLAVTVATPTTLPRPSPAASTTSIPRPSQVGHRSQEMDLNSTATYTSQNR 240
241 PRADPGIQRDPGSAFAQFPGVADVSLGLVPKEELTQSLEPVSLGDPNCKIDLSDLIDG 300
241 PRADPGIQRDPGSAFAQFPGVADVSLGLVPKEELTQSLEPVSLGDPNCKIDLSDLIDG 300
301 STSICKRRFRIOQLLADVAQALDIPAGPLMGVVOYGDNPATHFNLKTHNSRDLKTAI 360
301 STSICKRRFRIOQLLADVAQALDIPAGPLMGVVOYGDNPATHFNLKTHNSRDLKTAI 360
361 EKITQGGLSNVGRALISFVTKNFFSKANGNRSGAPNVMVMDGPTDKVBEASRLARES 420
361 EKITQGGLSNVGRALISFVTKNFFSKANGNRSGAPNVMVMDGPTDKVBEASRLARES 420
421 GINIPIITTEGAENKQVVEPNFANKAVCRTRNGFVSLHVQSWFGLHKTQLPLVKRQCD 480
421 GINIPIITTEGAENKQVVEPNFANKAVCRTRNGFVSLHVQSWFGLHKTQLPLVKRQCD 480
481 TDLRACKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVTNLTKEFBSIDTDRIGAVQYT 540
481 TDLRACKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVTNLTKEFBSIDTDRIGAVQYT 540
541 YEORLEFGDKYSKSPDILNAIKRVGWSGTTGAAINPALBQLFKSKPNKRKLMILI 600
541 YEORLEFGDKYSKSPDILNAIKRVGWSGTTGAAINPALBQLFKSKPNKRKLMILI 600
601 TDCRSYDDVRIPAMAAHLKGVITTAIGVAAWAAOELEVIATHPARDHSFPVDFDNLHQY 660
601 TDCRSYDDVRIPAMAAHLKGVITTAIGVAAWAAOELEVIATHPARDHSFPVDFDNLHQY 660
661 VPRIIQUICTEFNSQPRN 678
661 VPRIIQUICTEFNSQPRN 678

RESULT 15

US-09-989-735-179
; Sequence 179, Application US/09989735
; Publication No US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTVLTWKASVIEPLVLVTGHSNKTAKKIKRPFTVPQINCVDKAGKIIDPEPIV 60
Db 1 MRTVLTWKASVIEPLVLVTGHSNKTAKKIKRPFTVPQINCVDKAGKIIDPEPIV 60
Qy 61 KCPAGCQDPKHVYGTVDVYASVSSVCGAAVSGVLDNSGKILVRKVAQSGVKGYSNG 120
Db 61 KCPAGCQDPKHVYGTVDVYASVSSVCGAAVSGVLDNSGKILVRKVAQSGVKGYSNG 120
Qy 121 VQSLSPRWRESFIVLESKPKKGVTPSALYSSSKSPAAQAGETTAKYQRPPIGTTAQ 180
Db 121 VQSLSPRWRESFIVLESKPKKGVTPSALYSSSKSPAAQAGETTAKYQRPPIGTTAQ 180
Qy 181 PVTLMQLLAVTVAVATPTTLPRPSPAASTTSIPRPSQVHRSQEMDLWSTATYSSQNR 240
Db 181 PVTLMQLLAVTVAVATPTTLPRPSPAASTTSIPRPSQVHRSQEMDLWSTATYSSQNR 240
Qy 241 PRADPGIORQDPSCGAAPQKPGVADVSLGLVPKEELSTOSLBPVSLGDPNCKIDLFLIDG 300
Db 241 PRADPGIORQDPSCGAAPQKPGVADVSLGLVPKEELSTOSLBPVSLGDPNCKIDLFLIDG 300
Qy 301 STSICKERFRIQKQLLADVAQALDIPAGPLMGVVQYGDNPATFNLTHTNSRDLKTAI 360
Db 301 STSICKERFRIQKQLLADVAQALDIPAGPLMGVVQYGDNPATFNLTHTNSRDLKTAI 360
Qy 361 EKITQRGGLSNVGRAISPVTKNFTSKANGNSGAPNVVVVWVDGWPDKVEASRLARES 420
Db 361 EKITQRGGLSNVGRAISPVTKNFTSKANGNSGAPNVVVVWVDGWPDKVEASRLARES 420
Qy 421 GINIPTTIBGAANERQYVVEPNPANKAVCRKTGFSYLSHVQSWFGLHKTLPVKRUCD 480
Db 421 GINIPTTIBGAANERQYVVEPNPANKAVCRKTGFSYLSHVQSWFGLHKTLPVKRUCD 480
Qy 481 TDLRACSKTCLNSADIGFVIDGSSSVGTGNFTVLQFVTNLTKEFEISDTOTRIGAVQYT 540
Db 481 TDLRACSKTCLNSADIGFVIDGSSSVGTGNFTVLQFVTNLTKEFEISDTOTRIGAVQYT 540
Qy 541 YEQRLBFGFDKYSKPKDILNAIKRVYWSGGTGTGAANPALBQLFKSKSPKWKRLMILI 600
Db 541 YEQRLBFGFDKYSKPKDILNAIKRVYWSGGTGTGAANPALBQLFKSKSPKWKRLMILI 600
Qy 601 TDGHSYDDVRIIPANAAHLKGVITYAIGVAAQAQBELEVIATHPARDHSPFVDEPNLHOY 660
Db 601 TDGHSYDDVRIIPANAAHLKGVITYAIGVAAQAQBELEVIATHPARDHSPFVDEPNLHOY 660

Search completed: May 27, 2004, 16:49:26
Job time : 64 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 16:41:07 ; Search time 22 Seconds
(without alignments)
1604.708 Million cell updates/sec

Title: US-10-063-688-34

Perfect score: 3502

Sequence: 1 MRTVLTQKASVIEFLVLL.....QYVPRIIICTEFNSQPN 678

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1139	32.5	547	1 COCH_CHICK	O42163 gallus gall
2	1129.5	32.3	550	1 COCH_HUMAN	O43405 homo sapien
3	1113	31.8	552	1 COCH_MOUSE	Q62507 mus musculu
4	554	15.8	3124	1 CA1C_CHICK	P13944 gallus gall
5	552	15.5	3119	1 CA1C_MOUSE	Q60847 mus musculu
6	543.5	15.5	3063	1 CA1C_HUMAN	Q99715 homo sapien
7	504.5	14.4	3137	1 CA36_CHICK	P15989 gallus gall
8	501.5	14.3	496	1 CMAA_HUMAN	P21941 homo sapien
9	490	14.0	493	1 CMAA_CHICK	P05099 gallus gall
10	490	14.0	500	1 CMAA_MOUSE	P51942 mus musculu
11	471.5	13.5	3176	1 CA36_HUMAN	P12111 homo sapien
12	431.5	12.3	619	1 MTN4_HUMAN	O95460 homo sapien
13	412.5	11.8	624	1 MTN4_MOUSE	O89029 mus musculu
14	358.5	10.2	956	1 MTN2_HUMAN	O00339 homo sapien
15	337.5	9.6	956	1 MTN2_MOUSE	O08746 mus musculu
16	331	9.5	1888	1 CA1E_CHICK	P32018 gallus gall
17	329.5	9.4	2944	1 CA17_HUMAN	Q02388 homo sapien
18	280.5	8.0	929	1 CA1C_NOTVI	Q91145 notophthalm
19	279	8.0	3767	1 MUD3_CABEL	P34576 caenorhabdi
20	266	7.6	2813	1 VWF_HUMAN	F04275 homo sapien
21	262	7.5	481	1 MTN3_MOUSE	O35701 mus musculu
22	252.5	7.2	1019	1 CA16_CHICK	P20785 gallus gall
23	251	7.2	486	1 MTN3_HUMAN	O15232 homo sapien
24	248.5	7.1	452	1 MTN3_CHICK	O42401 gallus gall
25	248.5	7.1	2482	1 VWF_FIG	Q28833 sus scrofa
26	248	7.1	1329	1 KPL10_HUMAN	Q9P218 homo sapien
27	241.5	6.9	2813	1 VWF_CANFA	Q28295 canis fami
28	231	6.6	1152	1 ITAM_HUMAN	P11215 homo sapien
29	229	6.5	1153	1 ITAM_MOUSE	P05555 mus musculu
30	228	6.5	1028	1 CA16_HUMAN	P12109 homo sapien
31	228	6.5	1163	1 ITAK_HUMAN	P20702 homo sapien
32	226.5	6.5	1025	1 CA16_MOUSE	Q04857 mus musculu
33	219.5	6.3	1162	1 ITAD_HUMAN	Q13349 homo sapien

ALIGNMENTS

RESULT 1

ID	COCH_CHICK	STANDARD;	PRT;	547 AA.
AC	O42163;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Cochlin precursor (COCH-SB2).			
GN	COCH OR COCHSB2.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.			
RC	STRAIN=White leghorn; TISSUE=Basilar papilla;			
RX	MEDLINE=98409669; PubMed=9736748;			
RA	Heller S., Sheane C.A., Javed Z., Hudspeth A.J.;			
RT	"Molecular markers for cell types of the inner ear and candidate genes for hearing disorders."			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:11400-11405(1998).			
CC	- TISSUE SPECIFICITY: Expressed in inner ear structures; the spindle-shaped cells of the basilar papilla. Weaker expression found in the inferior and superior fibrocartilagenous plates and skeletal muscle.			
CC	- DEVELOPMENTAL STAGE: Specifically expressed at the late developmental stages in the cochlea.			
CC	- SIMILARITY: Contains 1 LCCL domain.			
CC	- SIMILARITY: Contains 2 VWF domains.			
CC	- DATABASE: NAME=Protein Spotlight;			
CC	NOTE=Issue 4 of November 2000;			
CC	WWW="http://www.expasy.org/spotlight/articles/spotlt004.html".			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; AF012252; AAC62253.1; -.			
DR	HSSP; P11215; 1JLM.			
DR	InterPro; IPR004043; LCCL dom.			
DR	InterPro; IPR002035; VWF_A.			
DR	Pfam; PF03815; LCCL; 1.			
DR	Pfam; PF00092; vwa; 2.			
DR	PRINTS; PR00453; VWFADOMAIN.			
DR	SMART; SM00603; LCCL; 1.			
DR	SMART; SM00327; VWA; 2.			
DR	PROSITE; PS50820; LCCL; 1.			
DR	PROSITE; PS50234; VWF; 2.			
KW	Glycoprotein; Repeat; Signal.			
FT	SIGNAL 1 19			

POTENTIAL.

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FT CHAIN 20 547 COCHLIN.
FT DOMAIN 24 117 LCCL.
FT DOMAIN 162 347 WFPA 1.
FT DOMAIN 364 534 WFPA 2.
FT DISULFID 30 46 BY SIMILARITY.
FT DISULFID 50 70 BY SIMILARITY.
FT CARBOHYD 218 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 547 AA; 59426 MW; 172724242641DF88 CRC64;

Query Match 32.5%; Score 1139; DB 1; Length 547;
Best Local Similarity 37.3%; Pred. No. 2.8e-67;
Matches 229; Conservative 104; Mismatches 165; Indels 116; Gaps 5;

Qy 60 VKPAGCDDPKHYGTDVYASVSGCAAVHSGVLSGKILVRKVGAGSGYKGSYN 119
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 44 VLPFANCPWQFYVFGDIYASVSGCAAIHRGVITNAGCAVAVQTLPGQENYPAVHAN 103
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 120 GVQSLSPRRRESFIVLESKPKGVTPYSALTYSSKSPRAQAQETTKAVQRPPIRTYA 179
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 104 GIQSVLSRWASSFSV-----TPGTNN 125
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 180 QPVTLMQLLAVTAVATPTTLPRPSPAASSTISIPRQSVGHRSGQEMDLKSTATYTSSQN 239
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 126 ---LALRAGRSVATARPAT----- 142
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 240 RPRADPGIORQDPGGAAPQKPVGADVSLGLVPKEELSTQSLPVSLSGDPNCKIDLSFLID 299
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 143 -----GKEPKKLEKKA-----GNKCKADIAFLID 168
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 300 GSTSIGKRRPRIKQLADVAQALDIPAGPLMGVGVQVGNPNATHFNLKHTNSRDLKTA 359
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 169 GSYNIGQRRENLQNFVGVKAVMLGIGTEGPHGVGVQVQASEHPKIEFYLKQNFPAKRYLFA 228
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 360 IEXTORGGISNVCRAISFVTKNPFSGKANGRCAPNVVMVDGWPDKVERASRLARE 419
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 229 IKELGFGGNSNTGKALKHAQKPFSENGARKGPKIIVVFLDGNFSDDLERAGIVARE 288
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 420 SGINIPITTEGAENEKQYVVEFNFAKAVCRNTGFGYSLHVSQWFLGHLTKLOPLVRVC 479
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 289 FGVNVFIVSAKPTTEELGMVQDIFGDKAVCRNNGFFSYQMPSPFQTKVVKELVQKLC 348
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 480 DTRLACSKTCLNSADIGFVIDGSSSVGTGNTFRVLQFVNLTKPEISDITDTRIGAVOY 539
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 349 SHEQMLCKTCTNSWNGFLIDGSSVGSNFRMLFEPISNVAKAFRISDTSKATVQF 408
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 540 TYQRLRPGDKYSSKPDILNAIKRVGVWSGGTGTGAALNPALEQLFKSKPKPKRK-LMI 598
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 409 TYDQRTSFSDYITTKKVLKSAIRNRYMSGTATGDAISFTTRNVFGPVGDGANKNPLV 469
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 599 LITDGRSYDDVRIIPAMAAHLKGVITYTAIGVAAAQAELEVIATHPARDHSFFVDFDNLH 658
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 469 ILTDGQSYDDVDRGPAVAAQKAGITVPSGVGVAMAPLDLDKQWASPRESHPTFTTREFGLE 528
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 659 QYVPRITONICTEP 672
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 529 QMVPDVIRGICKDF 542
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :

RESULT 2
COCH HUMAN STANDARD; PRT; 550 AA.
ID COCH HUMAN
AC 043405;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
Db Cochlin precursor (COCH-5B2) (UNQ257/PRO294).
GN COCH OR COCH5B2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Cochlea;
RX MEDLINE=98110569; PubMed=9441737;
RA Robertson N.G., Skvorak A.B., Yin Y., Weremowicz S., Johnson K.R.,
RA Kovatch K.A., Battey J.F., Bieber F.R., Morton C.C.;
RT "Mapping and characterization of a novel cochlear gene in human and in
RL mouse: a positional candidate gene for a deafness disorder, DFNA9.";
RN Genomics 46:345-354 (1997).
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandelin R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270 (2003).
RP N-GLYCOSYLATION, SUBCELLULAR LOCATION, AND PROTEOLYTIC PROCESSING.
RX MEDLINE=22727166; PubMed=12843317;
RA Robertson N.G., Hamaker S.A., Patriub V., Aster J.C., Morton C.C.;
RT "Subcellular localization, secretion, and post-translational
RT processing of normal cochlin, and of mutants causing the
RT sensorineural deafness and vestibular disorder, DFNA9.";
RL J. Med. Genet. 40:479-486 (2003).
RP STRUCTURE BY NMR OF 27-126.
RX MEDLINE=21458424; PubMed=11574466;
RA Liepinsh E., Trexler M., Kaikkonen A., Weigelt J., Banyai L.,
RA Pathy L., Otting G.;
RT "NMR structure of the LCCL domain and implications for DFNA9 deafness
RL disorder.";
RL EMBO J. 20:5347-5353 (2001).
RP VARIANTS DFNA9 GLY-66; GLU-88 AND ARG-117.
RX MEDLINE=99021390; PubMed=9806553;
RA Robertson N.G., Lu L., Heller S., Merchant S.N., Bayev R.D.,
RA McKenna M., Nadol J.B. Jr., Miyamoto R.T., Linthicum F.H. Jr.,
RA Neto J.F.L., Hudspeth A.J., Seidman C.E., Morton C.C., Seidman J.G.;
RT "Mutations in a novel cochlear gene cause DFNA9, a human nonsyndromic
RT deafness with vestibular dysfunction.";
RL Nat. Genet. 20:299-303 (1998).
RP VARIANT DFNA9 SER-51.
RX MEDLINE=99135917; PubMed=9931344;
RA de Kok Y.J.M., Bom S.J.H., Brunt T.M., Kemperman M.H.,
RA van Beusekom E., van der Velde-Visser S.D., Robertson N.G.,
RA Morton C.C., Huygen P.L.M., Verhagen W.I.M., Brunner H.G.,
RA Cremers C.W.R.J., Cremers P.P.M.;
RT "A pro51-to-ser mutation in the COCH gene is associated with late
RT onset autosomal dominant progressive sensorineural hearing loss with
RL vestibular defects.";
RL Hum. Mol. Genet. 8:361-366 (1999).
RP VARIANT DFNA9 ASN-109.
RX MEDLINE=21193177; PubMed=11295836;
RA Kamarinos M., McGill J., Lynch M., Dahl H.-H.M.;
RT "Identification of a novel COCH mutation, I109N, highlights the
RL similar clinical features observed in DFNA9 families.";
RL Hum. Mutat. 17:351-351 (2001).
RP ERRATUM.
RA Kamarinos M., McGill J., Lynch M., Dahl H.-H.M.;
RL Hum. Mutat. 18:547-548 (2001).
RN [9]
RP VARIANT DFNA9 THR-119.
RX MEDLINE=22873884; PubMed=14512963;

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[illegible]


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Qy 454 NGF-----YSLVQSWFGL-----HK 469
Db 362 TGYKILLTPMAAGSRHLSVGPQTTLINVRDLTADTEYQISVFAMKGLTSSEPTSMYEX 421
Qy 470 T---LQPLVKRVCDDRLACSKCLNSADIGFVIDGSSVGTGNFRTVLOFVNTLTKFE 526
Db 422 TQPKTKMKVQV-----ECSRGVDIKADIVFLVDSYSIGTANFVKVRAFLVLAKEFE 475
Qy 527 ISPTDTRIGAVQVYTYEQRLEPFGDKYSSKPDILNAIKRVGVWGSCTGTGAANPALBOLF 586
Db 476 ISPNRVQISLVQVSRDPHTFTLKEFNRVEDIIKAINTPFVPGSGTNTGKAMTYVREKIF 535
Qy 587 ---KXSEPNRKLMLITDGRSDYDVRIPMAHAHLKGVITYAIGVANAQEELEVIATHP 643
Db 536 VPKRGSNSVPKVMILITDGESSDAFRDPAIKLNSDVBPFAVGVDVAVRSELEIASPP 595
Qy 644 ARDHSFVDFDNLHGVVPRILIONICTEFNSQ 675
Db 596 AETHVTFVEDFDAPQISFVLVTQSCILRIDOE 627

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RESULT 6

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ID CA1C_HUMAN STANDARD; PRT; 3063 AA.
AC Q99715; Q99716;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Collagen alpha 1(XII) chain precursor.
GN COL12A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.
RX MEDLINE=97288521; PubMed=9143499;
RA Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R.,
RA Hudson D.L., Champlaud M.-F., Olsen B.R., Burgeson R.E.;
RT "Complete primary structure of two splice variants of collagen XII,
RT and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(IX)
RT collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human
RT chromosome 6q12-q13."
RL Genomics 41:236-242(1997).
CC -!- FUNCTION: Type XII collagen interacts with type I collagen-
CC containing fibrils, the COL1 domain could be associated with the
CC surface of the fibrils, and the COL2 and NC3 domains may be
CC localized in the pericellular matrix (By similarity).
CC -!- SUBUNIT: Trimer of identical chains each containing 190 kDa of
CC nontriple-helical sequences.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=The final tissue form of collagen XII may contain
CC homotrimers of either isoform Long or isoform Short or any
CC combination of isoform Long and isoform Short;
CC Name=Long;
CC IsoId=Q99715-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q99715-2; Sequence=VSP_001149;
CC -!- TISSUE SPECIFICITY: Found in collagen I-containing tissues: both
CC short and long isoforms appear in amnion, chorion, skeletal
CC muscle, small intestine, and in cell culture of dermal
CC fibroblasts, keratinocytes and endothelial cells. Only the short
CC isoform is found in lung, placenta, kidney and a squamous cell
CC carcinoma cell line.
CC -!- PTM: The triple-helical tail is stabilized by disulfide bonds at
CC each end (By similarity).
CC -!- PTM: Prolines at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains (By
CC similarity).
CC -!- PTM: O-glycosylation of isoform Long; glycosaminoglycan of
CC chondroitin-sulfate type (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH

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CC INTERRUPTED HELICES (FACIT) FAMILY.
CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC -!- SIMILARITY: Contains 4 VWFA domains.
CC -!- SIMILARITY: Contains 18 fibronectin type III domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U73778; AAC51244.1; --
CC EMBL: U73779; AAD40483.1; --
CC HSP: P02751; ITTF.
CC Genew: HGNC:2188; COL12A1.
CC MIM: 120320; --
CC GO: GO:0005595; C:collagen type XII; TAS.
CC GO: GO:0001501; P:skeletal development; TAS.
CC InterPro: IPR008160; Collagen.
CC InterPro: IPR008957; FN III-like.
CC InterPro: IPR003961; FN III.
CC InterPro: IPR003129; TSPN.
CC InterPro: IPR02035; VWFA.
CC Pfam: PF01391; Collagen; 4.
CC Pfam: PF00041; fn3; 18.
CC Pfam: PF02210; TSPN; 1.
CC Pfam: PF00092; vwa; 4.
CC PRINTS: PR00453; VWFADOMAIN.
CC SMART: SM00060; FN3; 16.
CC SMART: SM00210; TSPN; 1.
CC SMART: SM00327; VWA; 4.
CC PROSITE: PS50234; VWFA; 4.
CC Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
CC Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
CC -----
FT SIGNAL 1 24
FT CHAIN 25 3063
FT DOMAIN 25 114
FT DOMAIN 140 316
FT DOMAIN 333 426
FT DOMAIN 440 616
FT DOMAIN 630 721
FT DOMAIN 722 812
FT DOMAIN 813 903
FT DOMAIN 904 998
FT DOMAIN 999 1085
FT DOMAIN 1086 1178
FT DOMAIN 1199 1371
FT DOMAIN 1384 1473
FT DOMAIN 1474 1564
FT DOMAIN 1565 1652
FT DOMAIN 1654 1751
FT DOMAIN 1752 1842
FT DOMAIN 1843 1932
FT DOMAIN 1933 2023
FT DOMAIN 2024 2114
FT DOMAIN 2115 2202
FT DOMAIN 2203 2291
FT DOMAIN 2323 2496
FT DOMAIN 2520 2712
FT DOMAIN 2747 2898
FT DOMAIN 2899 2941
FT DOMAIN 2942 3044
FT DOMAIN 3045 3063
FT SITE 862 864
FT SITE 2779 2781
FT SITE 2895 2897
FT MOD_RES 2944 2944
FT MOD_RES 2947 2947
COLLAGEN ALPHA 1(XII) CHAIN.
FIBRONECTIN TYPE-III 1.
VWFA 1.
FIBRONECTIN TYPE-III 2.
VWFA 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 8.
VWFA 3.
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 10.
FIBRONECTIN TYPE-III 11.
FIBRONECTIN TYPE-III 12.
FIBRONECTIN TYPE-III 13.
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 15.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 17.
FIBRONECTIN TYPE-III 18.
VWFA 4.
TSP N-TERMINAL.
NONHELICAL REGION (NC3).
TRIPLE-HELICAL REGION
(COL2) WITH 1 IMPERFECTION.
NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION
(COL1) WITH 2 IMPERFECTIONS.
NONHELICAL REGION (NC1).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).

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FT MOD_RES 2950 2950 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 2959 2959 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 2965 2965 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 2968 2968 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 2971 2971 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 2983 2983 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 3000 3000 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 3003 3003 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 3014 3014 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 3023 3023 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 3026 3026 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 3029 3029 HYDROXYLATION (BY SIMILARITY).
FT CARBOHYD 700 700 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 798 798 O-LINKED (XYL. . .) (CHONDROITIN SULFATE)
FT CARBOHYD 889 889 O-LINKED (XYL. . .) (CHONDROITIN SULFATE)
FT CARBOHYD 981 981 O-LINKED (XYL. . .) (CHONDROITIN SULFATE)
FT CARBOHYD 1763 1763 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2206 2206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2528 2528 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2679 2679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 25 1188 Missing (in isoform Short).
FT SEQUENCE 3063 AA; 333189 MM; 75FEA78FA8E48293 CRC64;

Query Match 15.5%; Score 543.5; DB 1; Length 3063;
Best Local Similarity 27.7%; Pred. No. 4e-27;
Matches 172; Conservative 76; Mismatches 207; Indels 165; Gaps 16;

Qy 179 AQPVTLMQLLAVTAVATPTTLRPSPS-----AASSTTS-----IPRQSVGHRSEQMD 227
Db 46 AEPVDPVIGYRITV---DPTT---DPTKEFTLSATITELLSELVPEYEV----- 91
Qy 228 LWSATYTTSSQNRPADFCIQDPSGGAFOKPGVGDVSLGLVPKELSTQSLSPVSLGD 287
Db 92 -----VTITSYDEVESVPIQGLTITQGSSTKPV-----EKKPGKTEI 130
Qy 288 PNCKI-----DLSFLDGTSGIKRRFRITQKLLADVAQALDIPAGPLMGVQVQDNPAT 343
Db 131 QKCSVSAMTDLVFLVDGWSVGRNNPKYILDFIALVSAFDIGBEKTRVGQVQSSDRT 190
Qy 344 HFNLTHTNSRLKTAIKITQROGLSNVGRSAISFVTKNFFSKANGNRSGAPNVVVWVD 403
Db 191 EFNLYQYQORDELLAAIKKIPYKGGNTWTGDAIDYLVKNTFTESAGARVGPPEKVAIITD 250
Qy 404 GWPTDKVEARSLARESGINIFPIIEGA-AENEKQYVVP-----NEAN----- 447
Db 251 GKSQDEVEIPARELRNVGVVEFSLGKAADAKELQIASPTPSLNHVFNVANFPAIDVQIN 310
Qy 448 ---KAVCR-----TNGF----- 456
Db 311 ELISQCSGVDEQLGELVSGEEVPEPPSNLAMEVSSKYVKNLWNPSPVTVGYKVLTP 370
Qy 457 -----YSLHVSQSWFG-----LHKTLQPLVKRV 478
Db 371 MTAGSRQHALSVGPQTTLTVRDLSDADTEYQISVSAMKQWTSSEPTISIMEKT-QPMKQVQ 429
Qy 479 CDTDLASCKTCLNSADIGFVIDGSSVGTGFRVLPVNLTKTFEISLDDTDTRIGAVQ 538
Db 430 -----ECSRGVDIIRADIIVFLVDGYSIGIANFVKVRAFLVFLVKSFEISPNRVQISLVQ 483
Qy 539 YTEQRLRPGPKYSKPDILNAIKRVGWSGTSNGAINFALRQLP---KKSKPKKKK 595
Db 484 YSRDPHTETLKKTKVEDIIEALINTFPRGSGTNTGKANTVYREKIFVPSKGSNSVPK 543
Qy 596 LMLITDGRSYDDVRIPAMAHLKGVITYIAGVANAQAELEVIATHPARDSHFFVDEPD 655
Db 544 VMLITDGRSSDAPRDPALIKRNSDVEIFAVGVGDVAVRSELEALASPPAEATHVFTVEDFD 603
Qy 656 NLHQVVPRIQNICTEFNSQ 675

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Db 604 APQRISFELTOSICLRIBQE 623
RESULT 7
CA36 CHICK
ID CA36 CHICK STANDARD; PRT; 3137 AA.
AC P15989;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagen alpha 3(VI) chain precursor.
GN COL6A3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE OF 1-853 FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=91035630; PubMed=1977751;
RA Doliana R., Bonaldo P., Colombatti A.;
RT "Multiple forms of chicken alpha 3(VI) collagen chain generated by
RT alternative splicing in type A repeated domains.";
RL J. Cell Biol. 111:2197-2205(1990).
RN [2]
RP SEQUENCE OF 224-2871 FROM N.A.
RX MEDLINE=90212613; PubMed=2322559;
RA Bonaldo P., Russo V., Bucciotti F., Doliana R., Colombatti A.;
RT "Structural and functional features of the alpha 3 chain indicate a
RT bridging role for chicken collagen VI in connective tissues.";
RL Biochemistry 29:1245-1254(1990).
RN [3]
RP SEQUENCE OF 2871-3137 FROM N.A.
RX MEDLINE=90062147; PubMed=2584214;
RA Bonaldo P., Colombatti A.;
RT "The carboxyl terminus of the chicken alpha 3 chain of collagen VI is
RT a unique mosaic structure with glycoprotein Ib-like, fibronectin type
RT III, and Kunitz modules.";
RL J. Biol. Chem. 264:20235-20239(1989).
CC -!- FUNCTION: Collagen VI acts as a cell-binding protein.
CC -!- SUBUNIT: Trimers composed of three different chains: alpha 1(VI),
CC alpha 2(VI), and alpha 3(VI).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=At least 2 isoforms are produced;
CC Name=1;
CC IsoId=P15989-1; Sequence=Displayed;
CC -!- PTM: Prolines at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -!- SIMILARITY: Contains 12 WPEA domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M24282; AAA03201.1; -
CC PIR; A37797; A37797.
CC HSP; P12111; 2KMT.
CC InterPro; IPR008161; Clg helix.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR002223; Kunitz_BPTI.
CC InterPro; IPR002035; VWF A.
CC Pfam; PF01391; Collagen; 6.
CC Pfam; PF00041; fn3; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.

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DR Pfam; PF00092; vwa; 11.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00453; VWFADOMAIN.
DR ProDom; PD000007; Cig helix; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00327; VWA; 12.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0234; VWFV; 12.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Cell adhesion; Serine protease inhibitor; Collagen;
KW Signal; Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 3137
FT DOMAIN 26 2042
FT DOMAIN 2043 2379
FT DOMAIN 2380 3137
FT DOMAIN 38 212
FT DOMAIN 241 418
FT DOMAIN 444 623
FT DOMAIN 644 817
FT DOMAIN 842 1014
FT DOMAIN 1035 1207
FT DOMAIN 1239 1410
FT DOMAIN 1441 1621
FT DOMAIN 1641 1814
FT DOMAIN 1840 2029
FT DOMAIN 2407 2587
FT DOMAIN 2625 2821
FT DOMAIN 2945 3043
FT DOMAIN 3068 3137
FT SITE 2166 2172
FT SITE 2254 2259
FT SITE 2308 2309
FT SITE 2045 2047
FT SITE 2153 2155
FT SITE 2159 2161
FT ACT SITE 3082 3083
FT DISULFID 3072 3122
FT DISULFID 3081 3105
FT DISULFID 3097 3118
FT CARBOHYD 201 201
FT CARBOHYD 2084 2084
FT CARBOHYD 2436 2436
FT CARBOHYD 2563 2563
FT CARBOHYD 2581 2581
FT CARBOHYD 2683 2683
FT CARBOHYD 2867 2867
SQ SEQUENCE 3137 AA; ECB428578B536357 CRC64;

Query Match 14.4%; Score 504.5; DB 1; Length 3137;
Best Local Similarity 30.7%; Pred. No. 1.5e-24;
Matches 121; Conservative 87; Mismatches 155; Indels 31; Gaps 8;

QY 293 DLSFLDSTSTIGKRRPRIQKLLADVAQALDIDGAPGLMGVGVGDNPATFNKLKTN 352
DB 38 DIIFLVDSSWSIGKEHFQVLFRELVVVKALDVGNDPRFALVQSGNPHTEFQNTYPS 97

QY 353 SRDLKTAIEKITORGLSNVGRALSFVTNPFPSKANGNRS--GAPNVVVVMDGMPDKV 410
DB 98 NQDVLSHIANPMPYMGSGSKTGKGLYLEIENHLTKAAGSRASGVQVIVLTDGQSQDDV 157

QY 411 EASRLARESINIPFTIIEGAENEKQVYVPEPNFANKVCTNGTFYSLHFVQSPGLHKT 470
DB 158 ALPSSVLKSAHVNMIAGVQDAVEGELKEIASRPEDT-----HLFNLNFTALHGI 208

QY 471 LQPLVK--RVCTDRLACKS-----TCLNGADIGFVIDGSSVGTGNFRTVLOFVNLT 522
DB 209 VGDLVASVRTSWTPQAGAKGLVKDITQAQESADLIFLDGSDNIGSVNPFQAIRDELVNL 268

QY 523 KEFEISDITDTRIGAVQVYTYEORLEFGDKYSKPDILNAIKRVGYNSG-GTSTGAANFPA 581
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```
Db 269 ESLRVGAQIIHGVVQVSDQPRTEFALNSYSTKADVLDAVXALSFRGKEANTGALETV 328
QY 582 LEQLFKKSKPNK-----RKLMLITDGRSYDDVRIPANMAHLKGVITYTAIGVMAQBEL 636
DB 329 VENLFTQAGSGRIEAVPQILVLISGGSSDDIREGLAVKQASIFSPSIGVNLNADSABL 388
QY 637 EVIATHPARDSFFVDEFD--NLHQYVPRITONI 668
DB 389 QQIAT----DGSFAFTALDIRNLAARELLLPNI 418

RESULT 8
CAMA HUMAN
ID CAMA_HUMAN STANDARD; PRT; 496 AA.
AC P21941;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cartilage matrix protein precursor (Matrilin-1).
GN MATN1 OR CRTM OR CMP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91060568; PubMed=2246248;
RA Jenkins R.N., Osborne-Lawrence S.L., Sinclair A.K., Eddy R.L. Jr.,
RA Byers M.G., Shows T.B., Duby A.D.;
RT "Structure and chromosomal location of the human gene encoding
RT cartilage matrix protein.";
RL J. Biol. Chem. 265:19624-19631(1990).
CC -!- FUNCTION: Cartilage matrix protein is a major component of the
CC extracellular matrix of nonarticular cartilage. It binds to
CC collagen.
CC -!- SUBUNIT: Homotrimer.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 2 WVEA domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC EMBL; M55682; AAB38702.1; -
CC EMBL; M55675; AAB38702.1; JOINED.
CC EMBL; M55676; AAB38702.1; JOINED.
CC EMBL; M55677; AAB38702.1; JOINED.
CC EMBL; M55679; AAB38702.1; JOINED.
CC EMBL; M55680; AAB38702.1; JOINED.
CC EMBL; M55681; AAB38702.1; JOINED.
CC EMBL; M55683; AAB38702.1; JOINED.
CC PIR; A37979; A37979.
CC HSRP; P05099; LAQ5.
CC Genew; HGNC:6907; MATN1.
CC MIM; 115437; -
CC GO; GO:0005578; C:extracellular matrix; TAS.
CC GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
CC GO; GO:0006461; P:protein complex assembly; TAS.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR002035; VWF_A.
CC Pfam; PF00008; EGF; 1.
CC Pfam; PF00092; vwa; 2.
CC PRINTS; PR00453; VWFADOMAIN.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00327; VWA; 2.
CC PROSITE; PS00022; EGF_1; FALSE_NEG.
CC PROSITE; PS01186; EGF_2; 1.
```


RESULT 11
CA36 HUMAN STANDARD; PRT; 3176 AA.
ID P12111; Q16501;
AC P12111; Q16501;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Collagen alpha 3(VI) chain precursor.
GN COL6A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=90151612; PubMed=1689238;
RA Chu M.-L., Zhang R.-Z., Pan T.-C., Stokes D., Conway D., Kuo H.-J.,
Guanville R., Mayer U., Mann K., Deutzmann R., Timpl R.;
RT "Mosaic structure of globular domains in the human type VI collagen
alpha 3 chain: similarity to von Willebrand factor, fibronectin,
actin, salivary proteins and aprotinin type protease inhibitors.";
RL EMBO J. 9:385-393(1990).
RN [2]
RP REVISIONS.
RA Chu M.-L.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 2038-2373 FROM N.A.
RX MEDLINE=89066644; PubMed=3198591;
RA Chu M.-L., Conway D., Pan T.-C., Baldwin C., Mann K., Deutzmann R.,
Timpl R.;
RT "Amino acid sequence of the triple-helical domain of human collagen
type VI.";
RL J. Biol. Chem. 263:18601-18606(1988).
RN [4]
RP SEQUENCE OF 2092-2157 FROM N.A.
RX MEDLINE=88029444; PubMed=3665927;
RA Chu M.-L., Mann K., Deutzmann R., Pribula-Conway D.,
Hsu-Chen C.-C., Bernard M.P., Timpl R.;
RT "Characterization of three constituent chains of collagen type VI by
peptide sequences and cDNA clones.";
RL Eur. J. Biochem. 168:309-317(1987).
RN [5]
RP SEQUENCE OF 2092-2151 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=88161046; PubMed=3348212;
RA Weil D., Mattei M.-G., Passage E., van Cong N., Pribula-Conway D.,
Mann K., Deutzmann R., Timpl R., Chu M.-L.;
RT "Cloning and chromosomal localization of human genes encoding the
three chains of type VI collagen.";
RL Am. J. Hum. Genet. 42:435-445(1988).
RN [6]
RP SEQUENCE OF 32-236 FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=93054780; PubMed=1339440;
RA Zanussi S., Dollana R., Segat D., Bonaldo P., Colombatti A.;
RT "The human type VI collagen gene, mRNA and protein variants of the
alpha 3 chain generated by alternative splicing of an additional 5-end
exon.";
RL J. Biol. Chem. 267:24082-24089(1992).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 3107-3164.
RX MEDLINE=95182468; PubMed=7533217;
RA Arnoux B., Merigau K., Saludjian P., Norris K., Bjoern S.,
Olsen O., Petersen L., Ducruix A.;
RT "The 1.6 A structure of Kunitz-type domain from the alpha 3 chain of
human type VI collagen.";
RL J. Mol. Biol. 246:609-617(1995).
RN [8]
RP STRUCTURE BY NMR OF 3102-3164.
RX MEDLINE=96398604; PubMed=8805527;
RA Zweckstetter M., Czisch M., Mayer U., Chu M.-L., Zinth W., Timpl R.,

RA Holak T.A.;
RT "Structure and multiple conformations of the Kunitz-type domain from
human type VI collagen alpha3(VI) chain in solution.";
RL Structure 4:195-209(1996).
RN [9]
RP STRUCTURE BY NMR OF 3107-3164.
RX MEDLINE=97410331; PubMed=9265624;
RA Soerensen M.D., Bjoern S., Norris K., Olsen O., Petersen L.,
James T.L., Led J.J.;
RT "Solution structure and backbone dynamics of the human alpha3-chain
type VI collagen C-terminal Kunitz domain.";
RL Biochemistry 36:10439-10450(1997).
RN [10]
RP DISEASE.
RX MEDLINE=21987636; PubMed=11992252;
RA Demir E., Sabatelli P., Allamand V., Ferreiro A., Moghadaszadeh B.,
Makrelouf M., Topaloglu H., Echenne B., Merlini L., Guicheney P.;
RT "Mutations in COL6A3 cause severe and mild phenotypes of Ullrich
congenital muscular dystrophy.";
RL Am. J. Hum. Genet. 70:1446-1458(2002).
RN [11]
RP VARIANT EM GLU-1679, AND VARIANT HIS-2831.
RX MEDLINE=98204804; PubMed=95336084;
RA Pan T.-C., Zhang R.-Z., Pericak-Vance M.A., Tandan R., Fries T.,
Stajich J.M., Viles K., Vance J.M., Chu M.-L., Speer M.C.;
RT "Missense mutation in a von Willebrand factor type A domain of the
alpha 3(VI) collagen gene (COL6A3) in a family with Bethlem
myopathy.";
RL Hum. Mol. Genet. 7:807-812(1998).
CC - FUNCTION: Collagen VI acts as a cell-binding protein.
CC - SUBUNIT: Trimers composed of three different chains: alpha 1(VI),
alpha 2(VI), and alpha 3(VI).
CC - ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=PI2111-1; Sequence=Displayed;
CC Name=2;
CC IsoId=PI2111-2; Sequence=VSP 001172;
CC - PTM: Prolines at the third position of the tripeptide repeating
unit (G-X-Y) are hydroxylated in some or all of the chains.
CC - DISEASE: Defects in COL6A3 are a cause of Bethlem myopathy (BM)
[MIM:158810]. BM is a rare autosomal dominant proximal myopathy
characterized by early childhood onset (complete penetrance by the
age of 5) and joint contractures most frequently affecting the
elbows and ankles.
CC - DISEASE: Defects in COL6A3 are a cause of Ullrich congenital
muscular dystrophy (UCMD) [MIM:254090]; also known as Ullrich
scleroatonic muscular dystrophy. UCMD is an autosomal recessive
congenital myopathy characterized by muscle weakness and multiple
joint contractures, generally noted at birth or early infancy. The
clinical course is more severe than in Bethlem myopathy.
CC - SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC - SIMILARITY: Contains 1 fibronectin type III domain.
CC - SIMILARITY: Contains 12 VWFA domains.
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CC -----
CC EMBL; X52022; CAA36267.1; -
CC EMBL; X06196; CAA29557.1; -
CC EMBL; M20778; -; NOT ANNOTATED_CDS.
CC EMBL; M27449; AAA52057.1; -
CC EMBL; SA9432; AAA24261.1; -
CC PIR; A59140; CGRUJA.
CC PDB; 1KNT; 01-NOV-94.
CC PDB; 2KNT; 15-MAY-97.
CC PDB; 1KUN; 12-NOV-97.
CC PDB; 1KTH; 28-AUG-02.

DR Genew; HGNC:2213; COL6A3.
 DR MIM; 120250; -
 DR MIM; 158810; -
 DR MIM; 254090; -
 DR GO; GO:0005589; C:collagen type VI; TAS.
 DR GO; GO:0007537; P:muscle development; TAS.
 DR InterPro; IPR008161; C1g helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR InterPro; IPR002035; WFA_A.
 DR Pfam; PF01391; Collagen_5.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR Pfam; PF00092; WFA; 11.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRINTS; PR00453; WFA_DOMAIN.
 DR ProDom; PD000007; C1g helix; 2.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00060; FN3; 1.
 DR SMART; SM00131; KU; 1.
 DR SMART; SM00327; WFA; 12.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR PROSITE; PS0234; WFA; 12.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 KW Glycoprotein; Cell adhesion; Serine protease inhibitor; Collagen;
 KW Signal; 3D-structure; Disease mutation; Polymorphism;
 KW Alternative splicing.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 3176 COLLAGEN ALPHA 3(VI) CHAIN.
 FT DOMAIN 26 2038 NONHELICAL REGION.
 FT DOMAIN 2039 2375 TRIPLE-HELICAL REGION.
 FT DOMAIN 2376 3176 NONHELICAL REGION.
 FT DOMAIN 39 213 WFA 1.
 FT DOMAIN 242 419 WFA 2.
 FT DOMAIN 445 620 WFA 3.
 FT DOMAIN 639 816 WFA 4.
 FT DOMAIN 837 1009 WFA 5.
 FT DOMAIN 1029 1205 WFA 6.
 FT DOMAIN 1233 1404 WFA 7.
 FT DOMAIN 1436 1609 WFA 8.
 FT DOMAIN 1639 1812 WFA 9.
 FT DOMAIN 1838 2024 WFA 10.
 FT DOMAIN 2024 2581 WFA 11.
 FT DOMAIN 2619 2815 WFA 12.
 FT DOMAIN 2987 3076 FIBRONECTIN TYPE-III.
 FT DOMAIN 3107 3176 BPTI/KUNITZ INHIBITOR.
 FT SITE 2040 2042 CELL ATTACHMENT SITE.
 FT SITE 2136 2138 CELL ATTACHMENT SITE.
 FT SITE 2148 2150 CELL ATTACHMENT SITE.
 FT SITE 2154 2156 CELL ATTACHMENT SITE.
 FT SITE 2370 2372 CELL ATTACHMENT SITE.
 FT ACT SITE 3121 3122 REACTIVE BOND.
 FT DISULFID 3111 3161
 FT DISULFID 3120 3144
 FT DISULFID 3136 3157
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
 Query Match 13.5%; Score 471.5; DB 1; Length 3176;
 Best Local Similarity 30.9%; Pred. No. 2.3e-22;
 Matches 122; Conservative 86; Mismatches 149; Indels 39; Gaps 12;
 QY 293 DLSFLDSTGIGKRRPRIQKQLADVAQALDIDGAPGLMGVVOYGDNPATFHLKHTN 352
 DB 39 DIFLVDSSTWIGEEHFLVREFLDYVVKSLAVGENDHFAVLQVQNGPHTEFLNTYRT 98
 QY 353 SRDLKTALEIKTORGLSNVGRASISFTYTKNFFSKANGNRS--GAPNVVVVMDGPTDKV 410
 DB 99 KQEVLSHNSNYSYIGTGTQKGLLEYIMQSHLTKAAGSRAGDGVQVIVLWLTGHSKDL 158
 QY 411 EASRLARESINIPFTIEGAENE-KQYVVEPNFANKVCRGTNGFSLH--VQSWFG- 466
 DB 159 ALPSAELKSADVNVFAIGVEDADEGALKXIASEP--LNMHMFLENFTSLHDIVGNLVSC 216

467 LHKTQLPVRKVCVDTDRILACSKTCNLGADIGFVIDGSSVGTGNFRFTVLQFTNLTKEPE 526
 DB 217 VHSVSP--ERAGDTETLK-DITAGDSADIIFLIDGSNNTGTVNFAVTLDFLVNLEKL 273
 QY 527 ISDTDTIGAVOYTVBORLRFQDKYSKPKDILNAIKRVGYWSGG--TSTGAALPALBO 584
 DB 274 IGTOQIRVGVVQVSDSPRTMFSLTYSKAQVLGAVKALGF-AGGELANIGLALDFVVEN 332
 QY 585 LFKKSKPNK-----RKLMLITDGRSYDDVRIPAMAHLKGVITVYVIAGVMAAQBELEVI 639
 DB 333 HFTRAGCSRVEEGVQVPLVLISAGPSSDEIRYGVVVALKQASVFSFGLGAQAASRAELQHI 392
 QY 640 ATHPARDSFPVDFDKLHQVVPRIIIONICTEFNS 674
 DB 393 ATD-----DNLVFTVP-----EFS 407

RESULT 12
 MTN4 HUMAN
 ID MTN4 HUMAN STANDARD; PRT; 619 AA.
 AC O95460; Q9H1F8; Q9H1F9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Matrilin-4 precursor.
 GN MATN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBT_Taxid=9606;
 RN [1]
 RC TISSUE=Embryonic kidney;
 RP MEDLINE=99043241; PubMed=9827539;
 RA Wagener R., Kobbe B., Paulsson M.;
 RT "Genomic organisation, alternative splicing and primary structure of
 human matrilin-4";
 RL FEBS Lett. 438:165-170(1998).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 Jones M., Stavrides G., Almeida J.P., Babbage A.K., Begguley C.L.,
 Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
 Clegg S., Cobley V.E., Collier R.E., Connor R.R., Corby N.R.,
 Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 Lehaealao M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
 Mine S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20";
 RL Nature 414:865-871(2001).
 CC -!- FUNCTION: Major component of the extracellular matrix of
 cartilage.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS;

Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1;
IsoId=095460-1; Sequence=Displayed;
Name=2;
IsoId=095460-2; Sequence=VSP 001400;
-!- TISSUE SPECIFICITY: Embryonic kidney, lung and placenta.
-!- SIMILARITY: Contains 4 EGF-like domains.
-!- SIMILARITY: Contains 2 VWF domains.

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EMBL; AJ007581; CAA07569.1; -;
EMBL; AL021578; CAC18104.1; -;
EMBL; AL021578; CAC18105.1; -;
HSSP; P00736; LAPQ.
Genew; HGNC:6910; MATN4.

MIM; 603897; -;
GO; GO:0005576; C:extracellular; TAS.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR002035; VWF_A.

Pfam; PF00008; EGF; 4.
Pfam; PF00092; vwa; 2.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00179; EGF CA; 1.
SMART; SM00327; VWA; 2.
PROSITE; PS00010; ASX HYDROXYL; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS02334; VWF_A; 2.

EGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil;
Alternative splicing.

SIGNAL 1 18 BY SIMILARITY.
CHAIN 19 619 MATRILIN-4.
DOMAIN 34 213 VWFA 1.
DOMAIN 215 253 EGF-LIKE 1 (INCOMPLETE).
DOMAIN 254 294 EGF-LIKE 2.
DOMAIN 295 335 EGF-LIKE 3.
DOMAIN 336 376 EGF-LIKE 4.
DOMAIN 384 559 VWFA 2. COILED COIL (POTENTIAL).
DOMAIN 594 618 BY SIMILARITY.
DISULFID 219 230 BY SIMILARITY.
DISULFID 226 239 BY SIMILARITY.
DISULFID 258 269 BY SIMILARITY.
DISULFID 265 278 BY SIMILARITY.
DISULFID 280 293 BY SIMILARITY.
DISULFID 299 310 BY SIMILARITY.
DISULFID 306 319 BY SIMILARITY.
DISULFID 321 334 BY SIMILARITY.
DISULFID 340 351 BY SIMILARITY.
DISULFID 347 360 BY SIMILARITY.
DISULFID 362 375 BY SIMILARITY.
CARBOHYD 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
VARSPPLIC 215 GHDQCAEGHGCHQCVCNVAWAMFHCCTCNPGYKLAADNRSS
-> A (in isoform 2).
/FTID=VSP 001400.
R -> S (IN REF. 1).
M -> NL (IN REF. 1).

SEQUENCE 619 AA; 68190 MW; 2FICE3C9CC54B5D CRC64;

Query Match 12.3%; Score 431.5; DB 1; Length 619;
Best Local Similarity 23.7%; Pred. No. 8.8e-21;
Matches 131; Conservative 70; Mismatches 191; Indels 161; Gaps 12;

QY	280	LEP-----VSLGDPNC---KIDSLFLIDGSTSIGKRRFRIQKQLADVAQAALDIPAGPLM 332
Db	14	LQWETQLQLTGPTRCHTGLDLVFDVSSRSRPPFETMRQFLMGLLGLNGLVGNATRV 73
QY	333	GVQYGDNPATFNLKTHNSRDLTAKTEKTQRGGLSNVGRASIVFTKVPFSKANGNR- 391
Db	74	GVIQISSQVQVFPPLRAFSRRRDMERALDVLPLAQGTWTGLAIQYAMNVAEVAEGARP 133
QY	392	--SGAPNVVVVMDGWPPTDKVEEASRLARESGINIFFITIEGA-----AENKQ 438
Db	134	PEERVPRAVITDGRPODRAEVAQAARAGIBIYAVGVQADVGSLRAMASPPLDHVV 193
QY	439	YVVE-----PNFANKAVCRNNGFVSLH--VQSWFGLHKTLOPLVKRVCDT-- 481
Db	194	FLVSEFDLIOBFGLOFQRLCGKQCAEGHGHGCHQCVCNVAWAMFHCCTCNPGYKLAADNKS 253
QY	482	--DRLA-----CSKTCLNS-----ADIGFV----- 499
Db	254	SIDLCAEGTHGCHHCVCNSPGSYFCHQVGVLPQDQSCRAIDYCSFGNHSCHQECVST 313
QY	500	----- 499
Db	314	EGPRCHCREGHDLPQDGRSCQVRDLGNDVDRGCEFCQVSEGLSVRCLCPEGRLQADGK 373
QY	500	-----IDGSSSVGTCNFTVLOFVTLNLTKEPEISDTDTIGAVQTYEOR 544
Db	374	SCNRCREGHVDLVLDVLDGSKSVRPQNFELVKRFVFNQIVDFLDVSPGEGTVGLVQFSSVR 433
QY	545	LEFGDKYSSKPDILNAIKRVYWSGGTGTGAANFALBOLPKK---SKP---NKKKLM 598
Db	434	TEPPLGRYGTAAEVQAVLAVYEMRGTTWGLALHMHVSESEAGQAPRALNVPVGL 493
QY	599	LITDGRSYDDVRIPAMAHLKVITYAIGVAAQBELEVIATHPARDHSFFVDEPDNLH 658
Db	494	VPTDGRSQDDISVWAARAKEGIVMVYGVGVKVAEARELREIASPAELHVSVPADRGTM 553
QY	659	QYVPRIIQNICR 671
Db	554	HLLENLRGSIQPR 566
RESULT 13		
MTN4 MOUSE		
ID	MTN4 MOUSE	STANDARD; PRT; 624 AA.
AC	O89029; O89030; O9QMS3;	
DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	15-MAR-2004 (Rel. 43, Last annotation update)	
DE	Matrilin-4 precursor (MAT-4).	
GN	MATN4.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND VARIANTS.	
RC	STRAIN=C57BL/6J, and CD-1; TISSUE=Petal;	
RX	MEDLINE=98442849; PubMed=9771906;	
RA	Wagener R., Kobbe B., Paulson M.;	
RT	Matrilin-4, a new member of the matrilin family of extracellular	
RL	matrix proteins.;	
RL	FEBS Lett. 436:123-127(1998).	
RN	[2]	
RP	SEQUENCE FROM N.A. (ISOFORM LONG).	
RC	STRAIN=C57BL/6J; TISSUE=Mammary gland;	
RX	MEDLINE=22388257; PubMed=12477932;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Pabey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A., RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [3]

RN SEQUENCE OF 218-257 FROM M.A. MEDLINE=99043241; PubMed=9827539; RA Wagener R., Kobbe B., Paulsson M.; RT "Genomic organisation, alternative splicing and primary structure of human matrilin-4.", RL FEBS Lett. 438:165-170 (1998).

CC -I- FUNCTION: Major component of the extracellular matrix of cartilage.

CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- ALTERNATIVE PRODUCTS:

CC Name=Long; IsoId=O89029-1; Sequence=Displayed;

CC Name=Short; IsoId=O89029-2; Sequence=VSP_001401;

CC -I- TISSUE SPECIFICITY: Lung, brain, sternum, kidney and heart.

CC -I- DEVELOPMENTAL STAGE: The short isoform was detected in 7 weeks old mice but not in developing mice (19.5 dpc embryos or in 2, 8, and 21 days old animals).

CC -I- SIMILARITY: Contains 4 EGF-like domains.

CC -I- SIMILARITY: Contains 2 VWFA domains.

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DR EMBL; AJ006140; CAA06889.1; -

DR EMBL; AJ006140; CAA06890.1; -

DR EMBL; BC036558; AAM36558.1; -

DR EMBL; AJ010984; CAA09451.1; -

DR HSSP; P00736; IAPQ.

DR MGD; MGI:1328314; Matn4.

DR InterPro; IPR00152; Asx_hydroxyl_s.

DR InterPro; IPR06209; EGF_like.

DR InterPro; IPR06210; IEGF.

DR InterPro; IPR002035; VWFA.

DR Pfam; PF00092; vwa; 2.

DR PRINTS; PR00453; VWFADOMAIN.

DR SMART; SM00181; EGF; 4.

DR SMART; SM00327; VWA; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 2.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS02034; VWFA; 2.

KW EGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil; Polymorphism; Alternative splicing.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 624 MATRILIN-4.

FT DOMAIN 36 215 VWFA 1.

FT DOMAIN 217 257 EGF-LIKE 1.

FT DOMAIN 258 298 EGF-LIKE 2.

FT DOMAIN 299 339 EGF-LIKE 3.

FT DOMAIN 340 380 EGF-LIKE 4.

FT DOMAIN 388 563 VWFA 2.

FT DOMAIN 590 623 COILED COIL (POTENTIAL).

FT	DISULFID	221	232	BY SIMILARITY.
FT	DISULFID	228	241	BY SIMILARITY.
FT	DISULFID	243	256	BY SIMILARITY.
FT	DISULFID	262	273	BY SIMILARITY.
FT	DISULFID	269	282	BY SIMILARITY.
FT	DISULFID	284	297	BY SIMILARITY.
FT	DISULFID	303	314	BY SIMILARITY.
FT	DISULFID	310	323	BY SIMILARITY.
FT	DISULFID	325	338	BY SIMILARITY.
FT	DISULFID	344	355	BY SIMILARITY.
FT	DISULFID	351	364	BY SIMILARITY.
FT	DISULFID	366	379	BY SIMILARITY.
FT	CARBOHYD	71	71	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	307	307	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPLIC	28	217	Missing (in isoform Short).
FT	VARIANT	319	319	/FTID=VSP_001401.
FT	VARIANT	346	346	A -> E (IN STRAIN C57BL/6J).
FT	VARIANT	624	624	G -> D (IN STRAIN C57BL/6J).
SEQ	SEQUENCE	624	AA; 68918	MW; DPA28D2C94B1A14P CRC64;

Query Match 11.8%; Score 412.5; DB 1; Length 624;
 Best Local Similarity 22.6%; Pred. No. 1.6e-19;
 Matches 125; Conservative 71; Mismatches 199; Indels 159; Gaps 9;

Qy	274	ELSTQSLFVSLGDPNCKIDLSFLIDGSTSGKRRFRIOKQLADVAQALDIGPAGPLWG	333
Db	20	ETQLQASAGPRCTNGP---LDLVMIDSSRVRPFETMRQPLVGLLSLSDVGLNATRVG	76
Qy	334	VVOYGDNPATFNKTHNSRDLTAETKIQRGGLSNVGRARISFVTKNPFPSKANGNRSG	393
Db	77	VIQSSQVQVFPFGAFSRREMERARAVPLAQGTMTGLAIQYANMVAFSEASGARPS	136
Qy	394	---APNVVVVMDGMPDKVEEASRLARESINFTTIEGAARNEKYVVEP-----	443
Db	137	BEVRPVLVIITDGRPDQDRAEVAQAARARGIRIYAVGVQDQVGSRLTMSAPPLDQHPV	196
Qy	444	-----NFANKVCRTNGFYSL-----	459
Db	197	LVSFDFLIQERLQFQGRLOGKOLCAELVHGCQHLVGNAPGTFYCACNSGYKLAPDNKNC	256
Qy	460	-----HVQSW-----FGLHKTLOPLVK	476
Db	257	LALDLCAGTHGCHLVCNSVDYPCRCRAGFALQDQDSCRAIDYCSFGNHSQCHECVS	316
Qy	477	-----RVC-----DTRD	483
Db	317	TLAGPQCKRCEHDLDPGRSCRVRDFCNGVDHGCEFCVSEGLSFHCLCPERRLOADG	376
Qy	484	LACSKTCLNSADICFVTDGSSVCTGTFVLTQVNTLTKEFEISDTTRIGAVQVTVBQ	543
Db	377	KSCDCRCEGHVDLVLDVSGSKSVRPQNFELVKRPVQIIVDFLDVSPGTRVGLVQFSRV	436
Qy	544	RLBFGPKYSSKPDILNAIKRAGVWSGTSGAINFALBQLFKK---SKP---NKRKLM	597
Db	437	RTEPPLGRYGTAAEVKQAVLAVETWERTGTGLALRHVHVSFSEAQGRPRDLNVPVVG	496
Qy	598	ILITDGRSYDDVRIPAMAHLKGVITYTAIGVAAQAELEVIATHPARDHSFVDFDNL	657
Db	497	LVFTDGRSQDDISVMAARAKEBGIVMVAVGKAVEELRELTASPSBLHVSYSDFDFTM	556
Qy	658	HQYVPRIIQICTE	671
Db	557	THLENLKGSICPE	570

RESULT 14
 MTN2 HUMAN
 ID MTN2 HUMAN STANDARD; PRT; 956 AA.
 AC 000339; Q9NS21;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Matrilin-2 precursor.

GN MATN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RX PubMed=1124542;
RA Muratoglu S., Krysan K., Balazs M., Sheng H., Zakany R., Modis L.,
RA Kiss I., Deak P.;
RT "Primary structure of human matrilin-2, chromosome location of the
RT MATN2 gene and conservation of an AT-AC intron in matrilin genes.";
RL Cytogenet. Cell Genet. 90:323-327(2000).
RN [2]
RP SEQUENCE OF 644-956 FROM N.A.
RX MEDLINE=97238663; PubMed=9083061;
RA Deak P., Piecha D., Bachrati C., Paulsson M., Kiss I.;
RT "Primary structure and expression of matrilin-2, the closest relative
RT of cartilage matrix protein within the von Willebrand factor type A-
RT like module superfamily.";
RL J. Biol. Chem. 272:9268-9274(1997).
RN [3]
RP SEQUENCE OF 244-956 FROM N.A.
RC TISSUE=Testis;
RA Duesterhoft A., Lauber J., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in matrix assembly (by similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=000339-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=000339-2; Sequence=VSP 001399;
CC -!- SIMILARITY: Contains 10 EGF-like domains.
CC -!- SIMILARITY: Contains 2 VWFA domains.
CC -----
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CC -----
CC EMBL; U69263; AAC51260.2; --
DR EMBL; AL137638; CAB70853.1; ALT_INIT.
DR HSSP; P01132; IEGF.
DR Genew; HGNC:6908; MATN2.
DR MIM; 602108; --
DR GO; GO:0005578; C:extracellular matrix; NAS.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002035; VWFA.
DR Pfam; PF00008; EGF; 10.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00327; VWFA; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 9.
DR PROSITE; PS01186; EGF_2; 9.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS02034; VWFA; 2.
KW EGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil;
KW Alternative splicing.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 956 MATRILIN-2.
FT DOMAIN 57 232 VWFA 1.
FT DOMAIN 238 278 EGF-LIKE 1.
FT DOMAIN 279 319 EGF-LIKE 2.
FT DOMAIN 320 360 EGF-LIKE 3.
FT DOMAIN 361 401 EGF-LIKE 4.

FT	DOMAIN	402	442	EGF-LIKE 5.
FT	DOMAIN	443	483	EGF-LIKE 6.
FT	DOMAIN	484	524	EGF-LIKE 7.
FT	DOMAIN	525	565	EGF-LIKE 8.
FT	DOMAIN	566	606	EGF-LIKE 9.
FT	DOMAIN	607	647	EGF-LIKE 10.
FT	DOMAIN	655	830	VWFA 2.
FT	DOMAIN	917	955	COILED COIL (POTENTIAL).
FT	DISULFID	242	253	BY SIMILARITY.
FT	DISULFID	249	262	BY SIMILARITY.
FT	DISULFID	264	277	BY SIMILARITY.
FT	DISULFID	283	294	BY SIMILARITY.
FT	DISULFID	290	303	BY SIMILARITY.
FT	DISULFID	305	318	BY SIMILARITY.
FT	DISULFID	324	335	BY SIMILARITY.
FT	DISULFID	331	344	BY SIMILARITY.
FT	DISULFID	346	359	BY SIMILARITY.
FT	DISULFID	365	376	BY SIMILARITY.
FT	DISULFID	372	385	BY SIMILARITY.
FT	DISULFID	387	400	BY SIMILARITY.
FT	DISULFID	406	417	BY SIMILARITY.
FT	DISULFID	413	426	BY SIMILARITY.
FT	DISULFID	428	441	BY SIMILARITY.
FT	DISULFID	447	458	BY SIMILARITY.
FT	DISULFID	454	467	BY SIMILARITY.
FT	DISULFID	469	482	BY SIMILARITY.
FT	DISULFID	488	499	BY SIMILARITY.
FT	DISULFID	495	508	BY SIMILARITY.
FT	DISULFID	510	523	BY SIMILARITY.
FT	DISULFID	529	540	BY SIMILARITY.
FT	DISULFID	536	549	BY SIMILARITY.
FT	DISULFID	551	564	BY SIMILARITY.
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FT	DISULFID	577	590	BY SIMILARITY.
FT	DISULFID	592	605	BY SIMILARITY.
FT	DISULFID	611	622	BY SIMILARITY.
FT	DISULFID	618	631	BY SIMILARITY.
FT	DISULFID	633	646	BY SIMILARITY.
FT	CARBOHYD	221	221	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	890	890	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPPLIC	861	879	Missing (in isoform Short).
FT	CONFLICT	356	356	/FTid=VSP_001399.
FT	CONFLICT	594	594	K -> E (IN REF. 3).
FT	CONFLICT	644	644	V -> E (IN REF. 3).
FT	CONFLICT	755	755	R -> G (IN REF. 2).
FT	CONFLICT	935	935	P -> L (IN REF. 3).
FT	CONFLICT	935	935	L -> F (IN REF. 2).
SQ	SEQUENCE	956 AA;	106840 MW;	826BF7347178FC80 CRC64;

Query Match 10.2%; Score 358.5; DB 1; Length 956;
Best Local Similarity 17.4%; Pred. No. 1e-15;
Matches 142; Conservative 80; Mismatches 189; Indels 405; Gaps 13;

QY	256	AFQKPVGADVGLVPEELSTQSLSPVSLGDPNCKIDLSPLDQSTSGKRFRIOKQL	315
DB	23	ARERSGRSISGRHARTHPTQALLES---SCENKRALVFTIDSSRSVNTHDYAKVKEP	79
QY	316	LADVAQALDIGPAGPLMGVQYGDNPATFNKLTHTNSRDLTAKIEKIQRGSLSNVGR	375
DB	80	IVDILQFLDIGDVTTRVGLLQYGVSTQNEFSLKTFKRSKSEVERAVRMHLSLTGTWGLA	139
QY	376	ISFVTKNFFSKANGN---RSGAPNVVVVMDGWPTDKVBEASRLARESGINIF	425
DB	140	IQYALNIAPSRAGARPURENVPVIMVTDGRPDQSVAEVAEAKARDTGILIFAGVGQV	199
QY	426	-PTIE--GAANEKQYVVEPNF	445
DB	200	DFNTLKSIGSFPHDHFVLFVANFSQITLTSVFQKCLCTAHMCSTLEHNCALHFCINPGS	259
QY	446	-----ANEKVC	452
DB	260	VYCRCKQGIYNSDQTTCRIQDLCAEDHNCQLCVNVPFSGVQCYSYALABDGRCV	319

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Qy 453 -----T 453
Db 320 AVDYCASENHGCEHCYNADSGSYLQCCHGEPALNPDKTKCTKIDYCASSNHGCHQHCVCNT 379
Qy 454 NGFYSLVHVSQWFGI-----HK--TLQP--- 473
Db 380 DDSYSCHCLGFTLNPDKTKCRINYCALNKPGEHCVCNNBESYYCRCHRGYTLDPNGK 439
Qy 474 ----- 473
Db 440 TCSRVDHCAQDHCCEQLCLNTWDSFVQCSEGFLLNEDLTKCSRVDYCLLSHGCHYSC 499
Qy 474 ----- 473
Db 500 VNMDRSPACQCEGHVLRSDGKCAKLDSCALDGHGCHSVCSSSEDSFVQCPEGYILRE 559
Qy 474 -----IV-----KRVCDTRLACS 487
Db 560 DGKTCRRKDVQCAIDHGCEHCIVNSDDSYTCECLVGFRLAEDGKRCRKKDYCKSTHHGCE 619
Qy 488 KTCLENSA-----DIGPVDIGSSSVCTGNFRTVLPQVT 519
Db 620 HICVNNNGNSYICKSEGFVLAEDGRRCKCTEGEPIDLVFVDGSKSLGHEFNFRVVKQFVT 679
Qy 520 NLTKPEPISDTRIGAVQYTYEQRLBFGFDKYSKPDILNAIKRVGVWSGGTSSTGAAIN 579
Db 680 GIIDSLISPKAARVGLQYSTQVHTFTLRNFNSAKDKKVAHMKYMGKSGMTGLAK 739
Qy 580 PALBQLPK---SIPNKKKL---MILITDGRSYDDVRIPAMAHLKGVITYTAIGVAAQAQ 633
Db 740 HMPERSFTQSGARPPFTRVRAAIVFTDGRAODVSEWASKAKANGITMYAVGVGKAIE 799
Qy 634 EELEVIATHPARDHSFFVDFEDNLHQVPRIONIC 669
Db 800 BELQEIASEPTNRKHLFYAEDPFTWDEISEKLRKGC 835

RESULT 15
MTN2_MOUSE STANDARD; PRT; 956 AA.
AC O08746;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Matrilin-2 precursor.
GN MATN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Limb;
RX MEDLINE=97238863; PubMed=9083061;
RA Deak F., Piecha D., Bachrati C., Paulsson M., Kiss I.;
RT "Primary structure and expression of matrilin-2, the closest relative
RT of cartilage matrix protein within the von Willebrand factor type A-
RT like module superfamily.";
RL J. Biol. Chem. 272:9268-9274 (1997).
CC CC -1- FUNCTION: Involved in matrix assembly (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Secreted.
CC CC -1- TISSUE SPECIFICITY: Detected in a variety of organs, including
CC CC calvaria, uterus, heart and brain, as well as fibroblast and
CC CC osteoblast cell lines.
CC CC -1- SIMILARITY: Contains 10 EGF-like domains.
CC CC -1- SIMILARITY: Contains 2 VWFA domains.
CC CC
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CC EMBL: U69262; AAC53163.1; -.
DR HSSP; P05099; 1AQS.
DR MED; MGI:109613; Matn2.
DR GO; GO:0005578; C:extracellular matrix; IDA.
DR InterPro; IPR00152; Abx_hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00008; EGF; 10.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00181; EGF; 10.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 7.
DR PROSITE; PS01186; EGF_2; 9.
DR PROSITE; PS02034; VWFA; 2.
KW EGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil.
FT SIGNAL 1 23
FT CHAIN 24 956
FT DOMAIN 57 232
FT DOMAIN 238 278
FT DOMAIN 279 319
FT DOMAIN 320 360
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FT DOMAIN 917 955
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FT DISULFID 577 590
FT DISULFID 592 605
FT DISULFID 611 622
FT DISULFID 618 631
FT DISULFID 633 646
FT CARBOHYD 221 221
FT CARBOHYD 890 890
SQ SEQUENCE 956 AA; 106779 MW; 3B4C22770B656EEB CRC64;
Query March 9.6k; Score 337.5; DB 1; Length 956;
Best Local Similarity 17.4k; Pred. No. 2.4e-14;
Matches 140; Conservative 75; Mismatches 177; Indels 413; Gaps 14;
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OM protein - protein search, using sw model

Run on: May 27, 2004, 16:47:44 ; Search time 52 Seconds
(without alignments)
4113.872 Million cell updates/sec

Title: US-10-063-688-34
Perfect score: 678
Sequence: 1 MRTLVTMKASVIMFLVLL.....QYPRITQICTFNSQPRN 678

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size: 6

Total number of hits satisfying chosen parameters: 8650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_protist.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	678	100.0	678	Q9UDN0	Q9udn0 homo sapien
2	411	60.6	693	Q96DM8	Q96dm8 homo sapien
3	259	38.2	656	Q96DT1	Q96dt1 homo sapien
4	57	8.4	652	Q95LI2	Q95li2 bos taurus
5	45	6.6	628	Q8BQ41	Q8bq41 mus musculus
6	45	6.6	650	Q8K047	Q8k047 mus musculus
7	45	6.6	650	Q9CYZ1	Q9cyz1 mus musculus
8	45	6.6	650	Q8VHI5	Q8vhi5 mus musculus
9	11	1.6	553	Q8AW56	Q8aw56 brachydanio
10	8	1.2	100	Q8H8Y2	Q8h8y2 oryza sativ
11	8	1.2	112	Q8G578	Q8g578 bifidobacte
12	8	1.2	174	Q8CB89	Q8cb89 mycobacteri
13	8	1.2	208	Q90ZY9	Q90zy9 brachydanio
14	8	1.2	230	O54667	O54667 streptococc
15	8	1.2	230	Q8KXQ1	Q8kxq1 streptococc
16	8	1.2	231	O86887	O86887 streptococc

17	8	1.2	231	2	Q9RIP2	Q9rip2 streptococc
18	8	1.2	231	2	Q9AMD3	Q9amd3 streptococc
19	8	1.2	285	16	Q92MJ9	Q92mj9 rhizobium m
20	8	1.2	359	1	Q47973	Q47973 halobacteri
21	8	1.2	368	17	Q9HPU7	Q9hpu7 halobacteri
22	8	1.2	382	12	Q83907	Q83907 ovine adeno
23	8	1.2	391	16	Q98HP8	Q98hp8 rhizobium l
24	8	1.2	394	16	Q97FB4	Q97fe4 clostridium
25	8	1.2	400	16	Q7UD27	Q7ud27 shigella fl
26	8	1.2	416	5	Q8IRF0	Q8irf0 drosophila
27	8	1.2	416	16	Q8FJ98	Q8fj98 escherichia
28	8	1.2	416	16	Q83LN3	Q83ln3 shigella fl
29	8	1.2	461	3	Q9HSC6	Q9hec6 neurospora
30	8	1.2	482	2	Q8RNG7	Q8rmg7 acetobacter
31	8	1.2	494	4	Q96IU6	Q96iue homo sapien
32	8	1.2	516	4	Q9H647	Q9h647 homo sapien
33	8	1.2	559	16	Q82I14	Q82i14 streptomyce
34	8	1.2	573	5	Q9GV07	Q9gv07 dugesia dor
35	8	1.2	686	5	Q9W013	Q9w013 drosophila
36	8	1.2	695	16	Q9CH87	Q9ch87 lactococcus
37	8	1.2	718	6	Q8HXH0	Q8hxo0 macaca fasc
38	8	1.2	763	5	Q960Y7	Q960y7 drosophila
39	8	1.2	892	16	Q99PX4	Q99px4 streptomyce
40	8	1.2	1078	5	Q9NDY3	Q9ndy3 leishmania
41	8	1.2	1464	5	Q9VX75	Q9vx75 drosophila
42	8	1.2	1464	5	Q96782	Q96782 drosophila
43	8	1.2	2197	5	Q9W016	Q9w016 drosophila
44	7	1.0	29	11	Q8VIF4	Q8vif4 mus musculu
45	7	1.0	34	4	Q9H3R8	Q9h3r8 homo sapien

ALIGNMENTS

RESULT 1
Q9UDN0
ID Q9UDN0 PRELIMINARY; PRT; 678 AA.
AC Q9UDN0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Similar to Coch-SB2.
GN WUGSC:H.NH0294J11.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Cordes M., Kallick J., Ames M.;
RT "The sequence of Homo sapiens BAC clone RP11-294L11.";
RN [3]
RP Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RA Waterston R.;
RP SEQUENCE FROM N.A.
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007363; AAF19243.1; -.
DR HSSP; P11215; 1JLM.
DR InterPro; IPR004043; LCCL.dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PRO0453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VVFA; 2.

Appendix B

